

1/52

#7

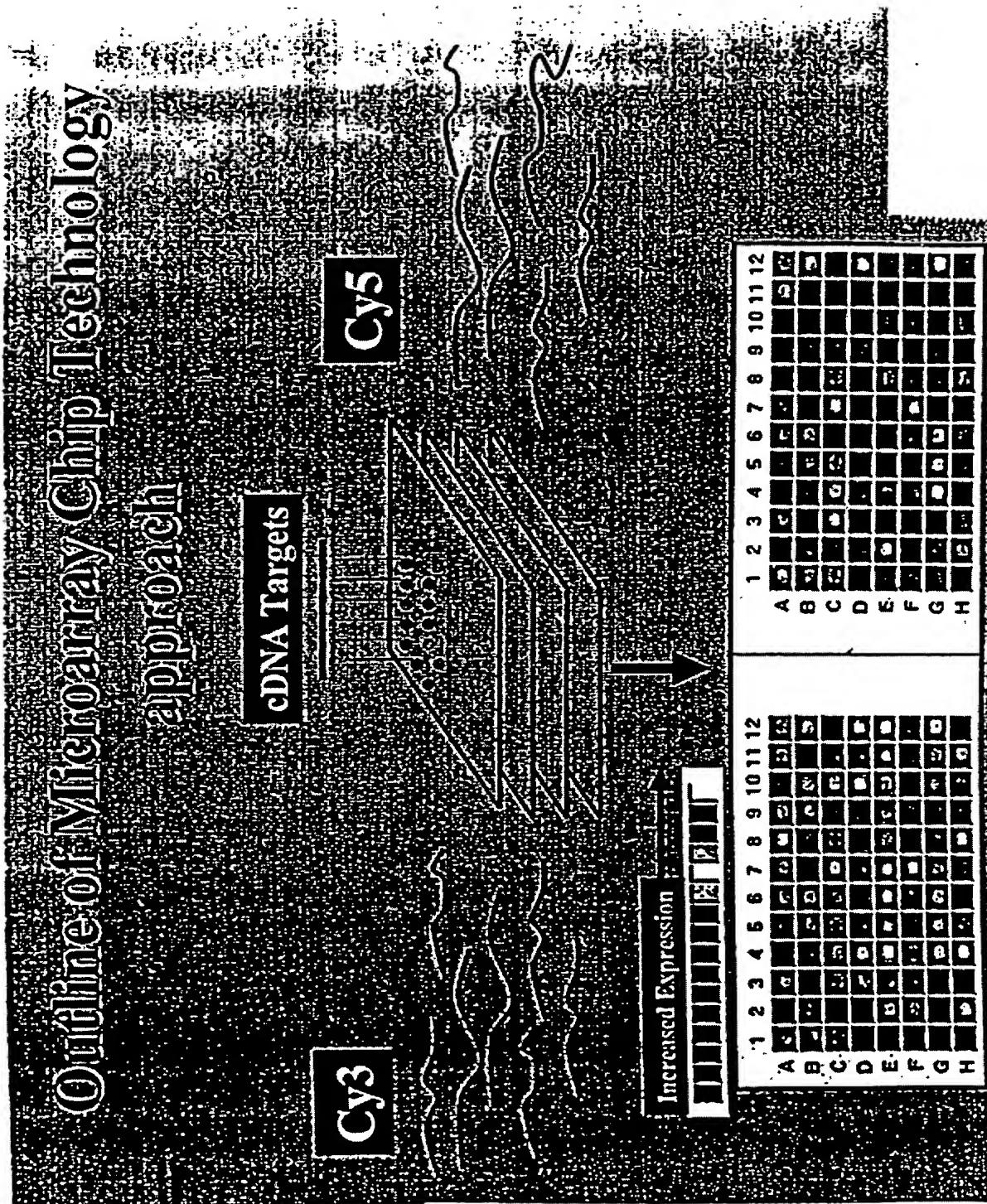
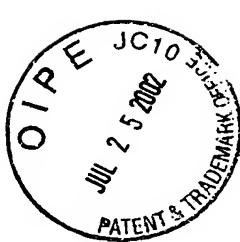


FIG. 1



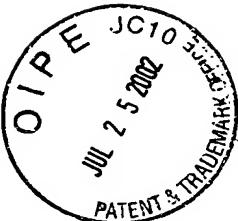
FIG. 2



LEUKEMIA/LYMPHOMA CHIP #3: PROBES USED IN ANALYSIS

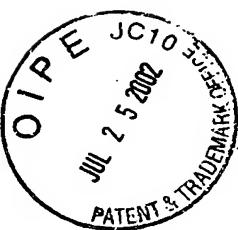
Cy3 Probe		Cy5 Probe	
Tissue	RNA#	RNA#	Tissue
Lymphoma, T cell	952	SPACT74	Kidney N
Lymphoma, B cell	955	SPACT81	Liver N
Lymphoma, B cell	953	SPACT78	Lung N
Lymphoma	916	SPACT42	Brain N
Lymphoma, Hodgkins	950	138598B	Skin N
Lymphoma, Hodgkins	950	SPACT49	Bone Marrow N
Lymphoma, B cell	CL151	888	PBMC resting
Lymphoma, T cell	904B	SPACT55	Stomach N
Lymphoma, Hodgkins see RNA 959	CL153	SPACT70	Thymus N
Lymphoma, B cell	CL152	SPACT75	Skeletal Muscle N
Lymphoma, B cell see RNA 958	CL155	SPACT73	Heart N
Lymphoma, B cell	844	243502B	Esophagus N
Lymphoma, B cell	958	1006	Colon N
Lymphoma, B cell	954	SPACT65	Small Intestine N
Lymphoma	960	779B	Trachea N
Lymphoma, T cell	957	S9327328	Bladder N
Lymphoma, B cell	914B		
Lymphoma, B cell	913		
Lymphoma, B cell	944B		
Lymphoma, B cell/failed	903		

GREEN: Tumor probes where gene expression would be desired.
 RED: Normal essential tissue probes where gene expression is to be avoided.
 BLACK : Normal tissue probes where gene expression is acceptable.



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High Dimensional Expression in Ovary 1 All Lymphomas > N compartment for lymphomas										All Human Samples > Ovarian Tumors											
Seq	ID	Element (30)	Parent	Marker	BP	Ratio	Signal 1		Signal 2		Marker	BP	Ratio	Signal 1		Signal 2		Marker	BP	Ratio	
							Mean	SD	Mean	SD				Mean	SD	Mean	SD				
10,510	RO429 C2	505	34	20.63	1.98	0.077	41	3026144	4	Highly expressed in Ovary 1 region	14 (1001537)	2	2	14 (1001537)	2	2	14 (1001537)	2	2	14 (1001537)	2
10,503	RO432 F1	505	263	14.19	0.98	0.054	5	13591113	4	Highly expressed in Ovary 1 region	14 (1001537)	2	2	14 (1001537)	2	2	14 (1001537)	2	2	14 (1001537)	2
10,532	RO438 E10	505	23	8.67	0.52	0.050	6	7705303	4	Hypothetical protein (BL0400)	77 (828674)	4	4	77 (828674)	4	4	77 (828674)	4	4	77 (828674)	4
10,487	RO448 A10	5052428	269	8.97	0.15	0.035	3	13723261	4	ADP-ribosylation factor binding protein (G2426)	63 (12804622)	3	3	63 (12804622)	3	3	63 (12804622)	3	3	63 (12804622)	3
10,534	RO450 C1	505	432	8.79	0.64	0.054	25	22465	4	Hypothetical protein (BL0400)	77 (828674)	4	4	77 (828674)	4	4	77 (828674)	4	4	77 (828674)	4
10,500	RO452 C3	528	468	6.62	0.4	0.050	6	10434649	4	Hypothetical protein (BL0400)	77 (828674)	4	4	77 (828674)	4	4	77 (828674)	4	4	77 (828674)	4
10,495	RO451 D10	505	210	5.89	0.51	0.050	4	15340577	4	Hypothetical protein (BL0400)	77 (828674)	4	4	77 (828674)	4	4	77 (828674)	4	4	77 (828674)	4
10,535	RO459 E11	519	365	5.69	0.45	0.073	3	13775153	4	Hypothetical protein (BL0400)	77 (828674)	4	4	77 (828674)	4	4	77 (828674)	4	4	77 (828674)	4
10,504	RO461 C1	505	218	5.76	0.32	0.053	17	5260594	4	DNase I site from RPA457961 on Chr. 13 (21-133)	63 (12804622)	3	3	63 (12804622)	3	3	63 (12804622)	3	3	63 (12804622)	3
10,488	RO468 D7	494	302	4.54	0.36	0.078	1	2573544	4	Chr. 18 (BL0400)	15 (1275019)	2	2	15 (1275019)	2	2	15 (1275019)	2	2	15 (1275019)	2
10,492	RO471 F8	505	326	3.94	0.30	0.077	3	7840557	4	Chr. 22 (BL0400)	15 (1275019)	2	2	15 (1275019)	2	2	15 (1275019)	2	2	15 (1275019)	2
10,507	RO473 H9	505	459	2.9	0.32	0.077	3	14520113	4	10 superfamily member transmembrane associated protein 2 (07742)	2 (1200584)	2	2	2 (1200584)	2	2	2 (1200584)	2	2	2 (1200584)	2
10,499	RO474 A9	528	538	1.69	0.26	0.064	17	14520020	4	10 superfamily member transmembrane associated protein 2 (07742)	2 (1200584)	2	2	2 (1200584)	2	2	2 (1200584)	2	2	2 (1200584)	2
10,498	RO471 F11	528	501	3.75	0.36	0.065	3	14150032	4	Hypothetical protein (BL0400)	61 (1105856)	2	2	61 (1105856)	2	2	61 (1105856)	2	2	61 (1105856)	2
10,503	RO474 MM	505	437	3.53	0.31	0.068	2	10407258	4	DNase I site from RPA467961 on Chr. 13 (21-133)	14 (1240452)	2	2	14 (1240452)	2	2	14 (1240452)	2	2	14 (1240452)	2
10,503	RO476 A3	505	610	3.27	0.30	0.068	0	11200589	4	DNase I site from RPA467961 on Chr. 13 (21-133)	14 (1240452)	2	2	14 (1240452)	2	2	14 (1240452)	2	2	14 (1240452)	2
10,515	RO476 F7	505	378	11.05	1.64	0.151	180	441354	4	Rearranged Ig kappa light chain variable region (07742)	260 (1367215)	10	10	271 (1367215)	10	10	271 (1367215)	10	10	271 (1367215)	10
10,523	RO478 E2	505	618	10.75	1.56	0.146	12	20773	4	B lymphocyte antigen CD20 (0110025)	10 (0880204)	2	2	10 (0880204)	2	2	10 (0880204)	2	2	10 (0880204)	2
10,518	RO479 C5	505	279	10.15	1.78	0.176	171	52711	4	Rearranged immunoprotein antigen (07742)	2 (12005772)	3	3	2 (12005772)	3	3	2 (12005772)	3	3	2 (12005772)	3
10,517	RO481 C6	505	417	10.95	1.58	0.156	12	20773	4	B lymphocyte antigen CD20 (0110025)	40 (1101776)	3	3	40 (1101776)	3	3	40 (1101776)	3	3	40 (1101776)	3
10,526	RO481 D2	505	615	9.95	1.17	0.118	12	20773	4	B lymphocyte antigen CD20 (0110025)	7 (11520147)	2	2	7 (11520147)	2	2	7 (11520147)	2	2	7 (11520147)	2
10,517	RO481 E10	505	17	10.15	1.26	0.156	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
10,517	RO481 F11	505	17	10.15	1.26	0.156	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
10,517	RO481 G12	505	17	10.15	1.26	0.156	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
10,517	RO481 H13	505	17	10.15	1.26	0.156	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
10,517	RO481 I14	505	17	10.15	1.26	0.156	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
10,517	RO481 J15	505	17	10.15	1.26	0.156	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
10,517	RO481 K16	505	17	10.15	1.26	0.156	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
10,517	RO481 L17	505	17	10.15	1.26	0.156	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
10,517	RO481 M18	505	17	10.15	1.26	0.156	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
10,517	RO481 N19	505	17	10.15	1.26	0.156	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
10,517	RO481 O20	505	17	10.15	1.26	0.156	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
10,517	RO481 P21	505	17	10.15	1.26	0.156	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
10,517	RO481 Q22	505	17	10.15	1.26	0.156	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
10,517	RO481 R23	505	17	10.15	1.26	0.156	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
10,517	RO481 S24	505	17	10.15	1.26	0.156	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
10,517	RO481 T25	505	17	10.15	1.26	0.156	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
10,517	RO481 U26	505	17	10.15	1.26	0.156	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
10,517	RO481 V27	505	17	10.15	1.26	0.156	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
10,517	RO481 W28	505	17	10.15	1.26	0.156	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
10,517	RO481 X29	505	17	10.15	1.26	0.156	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
10,517	RO481 Y30	505	17	10.15	1.26	0.156	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
10,517	RO481 Z31	505	17	10.15	1.26	0.156	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
10,517	RO481 A32	505	17	10.15	1.26	0.156	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
10,517	RO481 B33	505	17	10.15	1.26	0.156	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
10,517	RO481 C34	505	17	10.15	1.26	0.156	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
10,517	RO481 D35	505	17	10.15	1.26	0.156	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
10,517	RO481 E36	505	17	10.15	1.26	0.156	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
10,517	RO481 F37	505	17	10.15	1.26	0.156	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
10,517	RO481 G38	505	17	10.15	1.26	0.156	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
10,517	RO481 H39	505	17	10.15	1.26	0.156	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
10,517	RO481 I40	505	17	10.15	1.26	0.156	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
10,517	RO481 J41	505	17	10.15	1.26	0.156	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
10,517	RO481 K42	505	17	10.15	1.26	0.156	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
10,517	RO481 L43	505	17	10.15	1.26	0.156	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
10,517	RO481 M44	505	17	10.15	1																



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High Differential Expression in Group 1
All Lymphomas > N comparison for Lymphomas
Threshold: 3

Seq. #	Element (ID)	BP	Ratio	Mean		Genomic Description	Category	Compa	Intra	Inter	Number Ag	Disease	Geno	
				Signal 1	Signal 2									
10.576	RO43743	231	10.19	1.751	0.173	22	2184022	Anti-protein	21 (19704289)	3	0	3	0	0
10.576	RO43878	463	7.78	1.5	0.193	33	13270235	RO43878, cDNA: MIR725988N1323	57 (1325735)	1	0	2	0	0
10.565	RO43874	350	7.5	1.63	0.14	41	5566063	MIF2 suppressor (ISMT3)	18 (6003577)	1	0	1	1	1
10.560	RO43911	653	6.82	1.23	0.151	25	184271	poly(A)-binding protein, cytoplasmic 1 (PABPC1)	37 (1959602)	1	0	2	0	0
10.565	RO41047	375	6.5	0.559	0.148	0	0	hypothetical protein FLJ050321	80 (4753542)	1	0	0	0	0
10.560	RO40801	233	4.97	0.112	0.173	7	12003536	hypothetical protein FLJ050321, mRNA	48 (1959633)	5	0	0	0	0
10.560	RO42609	532	4.17	0.178	0.184	25	4506236	mRNA, seq. from clone RP11-2078B on Chr. 13	48 (1959630)	0	0	0	0	0
10.577	RO43787	483	3.57	0.47	0.116	4	1394577	Genomic, chromosome 6p21.3, HLA Class I region	4 (1026569)	0	0	0	0	0
10.566	RO41842	334	3.61	0.423	0.108	6	10440178	0	150 (1280426)	4	0	0	0	0
10.530	RO41010	208	3.9	0.135	0.112	3	5100077	elastase inhibitor factor 4A1	4 (12874065)	3	0	2	0	0
10.543	RO40897	302	3.87	0.509	0.131	1	4500154	RO43878, member RAS oncogene family	11 (1280069)	1	0	1	1	0
10.557	RO41612	546	3.35	0.148	0.108	6	1043762	MIF2 suppressor (ISMT3)	4 (5394077)	4	0	4	0	0
10.534	RO409012	543	3.71	0.569	0.153	4	1428035	non-biotin chromosomal protein FLG-14 gene	96 (1525443)	3	0	0	0	0
10.579	RO43912	342	3.68	0.513	0.14	1	6807703	hypothetical protein FLJ050321	22 (11155912)	10	0	0	0	0
10.563	RO43871	377	3.58	0.119	0.117	2	2588184	hypothetical protein FLJ050321	10 (11152091)	1	0	1	0	0
10.549	RO41011	358	3.48	0.347	0.1	0	0	mRNA, cDNA: MIR725988A010	148 (1429723)	14	0	12	5	0
10.559	RO41717	455	3.64	0.35	0.102	3	1042834	cDNA: FLJ21562 4.5, clone C00259420	38 (1247693)	3	0	2	0	0
10.534	RO41345	364	3.4	0.348	0.102	0	0	Chromosome 5 clone CTG-474A3	36 (1247693)	19	0	0	0	0
10.538	RO41781	369	3.29	0.114	0.126	0	0	cDNA: MIR725988A010	126 (1280010)	9	0	2	5	0
10.539	RO40704	184	3.17	0.321	0.101	2	6102950	regulation of O protein signaling (ROCS13)	90 (1178727)	9	0	0	0	0
10.566	RO43874	270	3.15	0.116	0.132	8	1043769	0	35 (2910364)	4	0	2	0	0
10.537	RO40899	662	3	0.321	0.107	3	2681020	mRNA, cDNA: MIR725988A010	117 (1233303)	6	0	2	0	0
0.2									19 (1181450)	2	0	0	0	0
10.568	RO43911	676	13.02	3.704	0.285	51	14126443	hypothetical protein FLJ050321	59 (1173482)	3	0	5	0	0
10.546	RO41038	408	10.85	4.03	0.38	1	10185402	DNase I hypersensitive site (HSS) on Chr. 13	33 (1073482)	3	0	5	0	0
10.564	RO40410	467	7.79	1.95	0.23	45	14141173	High-mobility group (nucleosomal chrom.) protein 2B (HMG-2)	239 (14053451)	8	0	5	0	0
10.570	RO40411	411	6.39	2.361	0.309	135	1353618	nucleolite 6	14 (1277710)	6	0	9	1	0
10.578	RO43877	430	5.35	3.701	0.59	0	0	MIF2 suppressor (ISMT3)	100 (1277710)	0	0	0	0	0
10.571	RO44184	420	4.09	0.065	0.221	44	5086863	hypothetical protein FLJ050321	3 (1280069)	8	0	9	0	0
10.542	RO40893	568	1.69	0.157	0.205	10	7022920	cDNA: FLJ10754 4.5, clone M72829300544	31 (19537449)	2	0	2	0	0
10.538	RO41173	469	3.22	1.776	0.543	1	6417076	cDNA: FLJ252628011224 (from clone M728293001224)	69 (12337261)	11	0	7	0	0
10.575	RO44510	303	3.26	1.963	0.607	42	1563063	nuclear sensitive element binding protein 1 (NSEP1)	115 (12776428)	11	0	9	10	0
10.571	RO44099	303	3.21	0.816	0.254	0	0	0	43 (2406528)	3	0	3	0	0

FIG. 6

Hematology therapeutic Ab candidates

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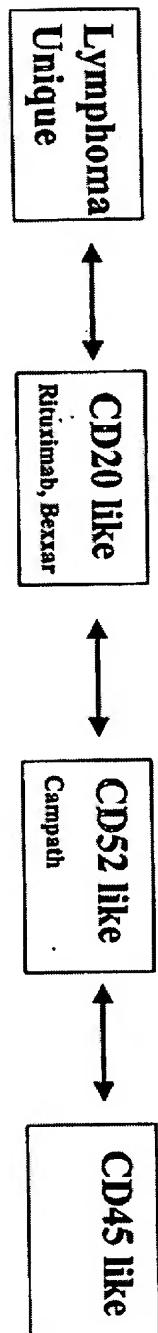
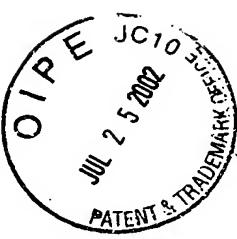


FIG. 7

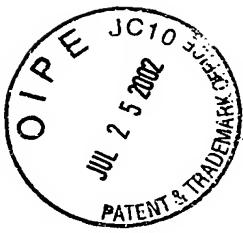


Identification of lineage specific markers and candidate lymphoma, leukemia and myeloma antigens

Gene	CD34+	CD18+	CD14+	CD2+	Ly	Hodgkin	Meloma	CLL*	AML
CD20	-	+++	-	-	+++	+	+	++	+/+
CD21	-	+	-	-	+++	++	+	+	-
TCL1	-	+	-	-	+++	+	-	++	-
Ly1448	-	+++	-	-	+++	+	-	++	-
Ly1452	-	+++	-	-	+++	+	+	+++	+/+
Ly1456	-	++	-	-	++	++	+++	-	-
Ly1464	-	+++	-	-	++	++	n.d.	n.d.	n.d.
Ly1483	-	+++	-	-	++	++	+	n.d.	-
Ly1458	-	+++	-	-	++	++	n.d.	n.d.	n.d.
Ly1481P	-	+++	-	-	++	+	n.d.	n.d.	n.d.
Ly1485P	-	+++	-	-	++	+	n.d.	n.d.	n.d.
Ly1480	+	++	++	+	++	++	n.d.	n.d.	n.d.
Ly1488	+	++	++	+	++	+	n.d.	n.d.	n.d.
Ly1484	+	++	+	+	+	++	n.d.	n.d.	n.d.
Ly1482	++	+++	++	+++	+++	++	n.d.	n.d.	n.d.
Ly1453	++	++	++	++	++	++	+++	+++	+++
Ly1449	++	+	-	-	+	+	+	+++	++
Ly1447	++	+++	+	+	++	++	n.d.	n.d.	n.d.
Ly1451	++	++	-	-	++	+	+	+++	+++
CD52	++	+++	++	++	++	++	n.d.	++	n.d.
CD45	+++	+++	+++	+++	+++	+++	n.d.	n.d.	n.d.

* single probe

Figure 8



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SECONDO
10,581

Ly1447 sequence:
CCTTCAAAGACTGGTGGGGTCCACCCACATTAGGGTGGACTTTGGTCTGCCACTGTGCCAGTTATCATTCTGGGATGGG
GGTACCTTACTCTCCCAATGAGAAAATTCTAAATTCTCTTGTGAGCCCTGGTGCCCTCCACCTTCTCANAACGTGCAATAGGG
CGTAGGCTCTTGTGGTGTGAGCTGACCTTCRGAAGACAGACTGTGAGCAGATTTTTCTTTAATCTGTAGGCCATGCTTGTGCTG
CTGTTCTTGTGACTTCACTGGCCATAAAAGCCGTT

SER 10 NO
10, 562

Ly1448 Sequence
CCGGGGTAGGACATTCAATGTCCTATCCACATTCTGAAAGGATAATTGTTATAGATTCCTACCTTCAAGGAATGC
TTATAATGATTATCTATAATCTCCACATTCCCACATTGTCATTAGAGAAATGGAATCAGTCAAACCCGTCTCCAGA
GTTTCCCTAGAGTTCTACCTGTTGTCATTATCTACATCTAGGAATCCTCCATCTTAATGTAAGCTTGGAGATCCGGCC
GGGGGGGGGACAGGTGACATGAGGACAAAAGCTGATCTGCTCTGCTAGTGGCTGGGGGATCACGGAAATGTCATCTTC
CTGGTAGACAGAGGGGCCACGGAAACAGTATGGGAAAAGAAAACCCAGCGTCCCTGTCAGCAGRCCTGGAGATCCCGACTG
CTGGAAAGAGGTAGTGGCGGCAATATGTCAGTGTAGCTGAGACATCTGACAG
CTCTGAGAGACCTGATGCTAGAGGAGACATCTGACAG

SECTION
10,583

Ly1449 Sequence
CCACATTGGAAATTCTGCACACAGGTCCCTGCTCCACCAACAGAGAGGCTCAGGGAGATTGTCAGGGACAAAGGAGACCTGGCCGGACACTCTGCAGGGAGGTGAGGCCCTGCCCCCATCTGTCATCCACATCTGGATTTGGCATCCCGAACGGCTCCTGAGGGAGGGAGAAGTGTGCTGATAAAAAAGGCCAAAATCACACAGAAAGAGAACAGAAAACCTCCACGGCACTTCTCATAGATGTGTCACGGTATTCTACGACACGGGCTGTGTGAAGACTCCCTCTGGAAAGTTACAGAAGGAAGGCCACCAAGATTCAAGCTCAGGCTCTTCTCAGATGCACTCACCACCTTACCCAAACCACTCTTCTCATATAATTTACACCTGTTTGTGGCTGGGAGCATATTGTGTTATTGATCTTCTAATTTCAGGGATTCTAAATGTGTTTGTGAGAATCTGTCACGACTCAGGATTCTGTCCTT

SECTION NO:
10, 584

Ly1451 Sequence
CTGCTGCTAAATACCTMTGAGAAAACCTGCTTCTATCTAAGGGGACCTACTTTTNTCNGGAATCTCAATACTTGGAAACAA
GAACCTCTTANACGGACCTTTGGCATTAATGAAATTGGGACCAACTGTAGGTTCCAGGACTAGAGGACCCAGCAATGCTCCCA
TGAACATCTCACCCAAATTACTCTGCTCAGGAAACGAGGTAACTGTAGGACAGCCGAGGCCCTTAGGCGCTTAGG
Ly1452 Sequence
AAAANACCAATAGCAGCCAAAACAGAACATTGTAAACAAAAACCAACAACTATGAGCCCTGTGCTTTAAACAGAGCTTCTGC
ATTCTTTTGAACATTAATGATATGCAATAAAGAGAAATATAGACCACTTCTTCTTCTTCAATATACAAATACCCAAATATCTAA
AACAATGTCACCAAAATAAGACCAAATCTGGTTATCATAGGCACTGTGAAACAGTCTTTTACAGTACTCAGGCGCA
TCATGGGGCTGCAAGGGCCACACTTCCAGAAGTTCTCCCTGCGTGTAGCTCCTCGCACACCCGGGGGCACTGGGAGGAG
GGAAGCACTGGTTGTGAAAGCAAGGCCCTGRCGCTGAAACATCTTACATGTGCTGTGCAAAATGGGAAGATGAGCAGTC
GTATTCCTGGCAAATTCAACAAATAAGGCCCCCTTCTTCTGACACGCTCACAGCCAGCCACATGTGCAAGGGAAAGCTTGAG
AAATGTCCTTGAGTAAGGTGCGAGCAGGCCCTTCTGATCTGACCCAGGTCTCAAGGGAGAAACAGGTGGAGCTCATCAG
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GGAAGAGCTGCTCTGATTTCTC

SEARCHED
10,586

Ly1453 Sequence
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TGAACCCAGCTAATTTATCTAGTGTGAAAARGAAATTATCATCTGCTACTGCTCTCTAAGAGTAGAC
TTAAAAATCATTAATGGAGGGAACTCTTGGAGATTAGTCGCTCATCTTGGGGCTCAGACRCCCCAAATCTATA
TATTGACCACTGGAAAGTTGATGATTGTTATCAAAATTCAAGCCCTATGGAAACCCCACTCTCATCTCTGGAAGATT
TTCACTGCTTCTTACAGCTTATTTGAAATTATTCAGCTACTCTGGGGCCACTTCAGAAACTCCATTGGGCTTTCAGATATT
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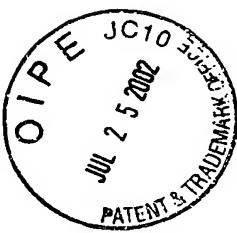
SEQ ID NO:
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 TTGAGCTCTGGAGGAGATTGACARANGGCGATGAAATCTCCATGCAAGGAGTATTCGGGGCCATCTTGGAGCTGTTG
 ATATGAGCAATGAGTACAGACAGATAGATAATTAGCAGTGACAATGAGTCTGGAGGAGCTACCTACCCACCTGCTCCCTTGTG
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SER ID ND:
10,588

SEQ ID NO:
10, 985

Ly1458 Sequence
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ATTCCTATTAAATTGGAAANCATNANAANATGGGTTGTTGAGTAANANATTAAAANAAATAAGCTTTTGTATCCCTG
CCCAACCCCCATCCAGGGGGNCACCTCCCTAAATACAATACATGCCAGGAAGTAAGNTGCCCCCTTCTGANGCCGNA
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19,590

6

Ly1464 Sequence
 aaagagagaactaatgg
 ccagaggacattggg
 atgggtgggatgtgtg

SERIUND

10, 591

Ly1480 Sequence
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ACAGCAGGGCTGCGTGTAGATGGGGAGAAGGCACGCTCAGATGAAAACATGCTGCAACGGATTTTCTACCACTG
AACACACTGTTCTGTGATAGAAAACGTGCGGCCCTGCTGGGGCAAGATATTACGGCCTCACTAGCCAGTGGAGATGC
CACCRGGCGGCCCTGCCCTGTGCTCTTGTAACTGTGCTAAAGAAGGACCATATAAGGTTAAAGGCACCTTACCTTATGG
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CTGCTCTAGAAGCTGGAGG

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10.942

Ly1482 Sequence
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GCTTATTCTCTGCACTGGACTGGAGACGGTCTCAGGGGGAGGAGCTCAGGTCTCCCTGGGCAAGACAGTGCCCCAGA
GAGTCCCCAGAACAGTGGACAGTCTGCTCTGTTCCATGCTCAGGCAGGGGAGAGAGTCGGTGG

SECTION

IC 5913

Ly1483 Sequence

GCTGGAGCTTCACTGTGAGTCCCTGAGGAGGCTCTTCCCGATCTGTACTGGTTTATCACGAGGAATGACACCTTGGGGAA
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GCTTGACAATGGCTGGGGGCCACAGCAGAATGGTGACACTCAATGTTACAGGAACATTCTCAGGAAACAGAACAGGCC
TTAACCRCTGGGGAATCACGGGCTGGTGSTCARCATCYTCGCTTGTGAGCTGCTGCTGCTGCTGCTGATTAACGGCAGG
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CAGG

SEARCHED

10.594

Ly1484 Sequence
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 GGGGGTTCTTCCTGAGGAGAGCTCAGGCCCCAGTCACCTCTGCAACCTCAGGCTGGCACTGTGTGTCAGGAGGCTCTG
 CTGGCTCTCTCTCTCTACCCATCTGAGCAGACAGCAGAAATATCTCCCTCTCATCACCAACCAAGGAGTGTGGTGTGCTG
 TCTGGACACGGCCAGAGCAGGTGCTACTGGGGGTTCTGGGCTCTCTGTCAAAGCAATGCTAACCTCCAGGCTCTG
 CGACTCAAGGCAAGGTTCTCTCCACTTGTCAGGCTCTGGGCTGGAGGCTGAGCCAGGGCTCTCTCTGCTGGCG
 CTGGAGGAACAGGACATCTCACATCTCAGCTCTCCAAACCCGGATCCGGCTTGTGACTCTGGGTGATGATGATCTGG
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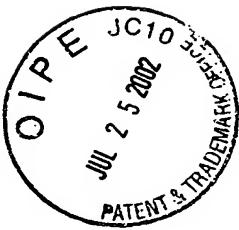
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Ly1485
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CCAGGAGGAGTAGTTAGAAGGTAACATGATAGTGGAAAGCACTTAAACATAGGCAAAATGTTTATATCAGGAATGATCAGG
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SEA IS ND:

10 Sept.

Ly1498
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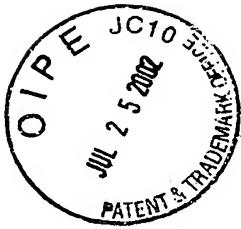
11/52

Figure 1a. Ly1464 full length DNA sequence (SEQ ID ND: 10,597)

1 gatgcaagga gatgagacag taaaatttac ttccctttt ctaatcttag aggtttcatg
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 121 tggcttctca tggcctggc cctctacctt tcccttggg tgctctgggt ggcccagatg
 181 ctactggctg ccagtttga gacgctgcag tggagggac ctgtctgcac tgaggagagc
 241 agctgccaca cggaggatga cttgactgtat gcaaggaaatg ctggcttcca gtcaggc
 301 tacactttca gtgaaccctt ccacctgatt gtgtctatg actggctgtat cttccaaagg
 361 ccageccaagc cagttttga aggggacatg ctggcttgc gtcggcaggc ctggcaagac
 421 tggccactga ctcaatcgtac cttctacgaa gatggcttag ctctgggtcc cccggggct
 481 aacaggaaat tctccatcac cgtggatcaa aaggcagaca gggggacta ccactgcagt
 541 ggcatttcc agagccctgg tcctgggatc ccagaaacag catctgtgt ggetatcaca
 601 gtccaaagaaat gttttccagc gccaatttcc agagctgtac cttcagctga accccaagca
 661 ggaaggccca tgaccctgg ttgtcagaca aagtggccc tgcagaggc agctggccgc
 721 ttccttttctt cttctatcaa ggtatggaaagg atatgtcaaa gcaggggctt ctctcagaa
 781 tttccagatcc ccacagcttc agaagatcac tccgggtcat actgggtgtga ggcagccact
 841 gaggacaacc aagtttggaa acagagcccc cagctagaga tcagagtgc ggtgtttcc
 901 agctctgtg caccctccac attgaatcca gtccttgc aatcagctgc tccaggaaact
 961 gctctgtggg aggccccctgg gctctgtgcct cccggccaa ccccatctt tgaggatcca
 1021 ggcttttttctt ctccctgtggg gatggccagat cttcatctgt atcaccagat gggccttctt
 1081 ctcaaacaca tgcaggatgt gagatgttcc ctcggtcacc tgctcatggg gtggaggaa
 1141 ttatctggcc accggaaagcc tgggaccaca aaggctactg ctgatagaa gtaaaacagtt
 1201 catccatgtat ctcactttaac cacccttcaata aatctgtatcc ttatcttctt ctccctgtcc
 1261 tgcacatata gataagtaat ttatcaatgtt gtcggcgtgt tttgttagaa taatgtatgt
 1321 aggtgatgtt aaataaaat tataatgtt gaaatgtttagaa ttttagtata atttgttatt
 1381 ctettttaaa acaacacaaat ttcgtgttcc agatggaaat ttatctatctg ttatatcgac
 1441 cagaatgttg tgatttaaaat agaactaattg gaaatggattt gaaatcagca gtcactgt
 1501 ggggcaattt tgccccccag agacatttgg gcaatgtttt gagacatttt ggtcattata
 1561 cttgggggggt tgggggatgg tggatgtgtt gtctactgg catccagtaa atagaagcca
 1621 ggggttccgc taaacatctt ataatgcaca gggcgttcc cccacaacgaa aaataatctg
 1681 gccccaaatg tcagttgtac tgatgttgg gcaatgttcc gtaatgaaac ccttaggtgtt
 1741 gggctcttgg aatggactttt gtcctttctt attattatctt tttccagcc tcaatcgat
 1801 attttttatctg acataccatg cttagtgcgg tgcctatggc tggttttag ttcttagttt
 1861 tataccctca aagccattt tggtaatc ctaatccca aggtgttgcg attaagaatgt
 1921 gggcccttttgg gaagtgtttaa gatcaggatg ctagccctt catgtttagg attagtgc
 1981 ttatctttaaa aggccccaga gagcttactc acccttccac catatgagga cgtggcaaga
 2041 agatgacatg tatgagaacc aaaaaacagc tggccaaatcaccgactt gtcgttgc
 2101 tggatcttggaa ctccacccat ccagaactat gagaataaa attctgttgc ttgtt

Figure 1b. Ly1464 protein sequence (SEQ ID ND: 10,598)

MKLGCVILMAWALYLSLGVLWVQMLLAASFETLQCEGPVCTEESSCHTEDDLTDAREAGFQVKAYTFSEPFHLIVSYDWLILQGPAKPV
 FEGDILVLRQQAQWDWPLTQVTFYRDGSALGPPGPNRFSITVVQKADSGHYNCSGIFQSPCPGIPETASVVAITVQELFPAPILRAVP
 SAEPQAGSPMTLSCQTKLPLQRSAARLLFSFYKDGRIVQSRGLSSEFQIPTASEDHSGSYCEAATEDQVWKQSPQLEIRVQGASSA
 APPTLNPAQPKSAAPGTAPEEAPGPLPPPPPSSEDPGFPSSPLGMPDPFLYHQWGLLKHMQDVRVLLGHILLMELRELSGHRKPGITKA
 TAE



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TMpred Report for Ly1464

Date:

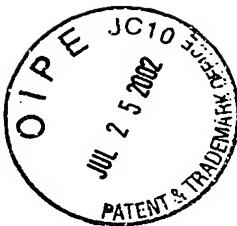
SEQ ID NO: 10,598

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DLTDAREAGFQVKAYTFSEPFHLIVSYDWLILQGPAKPVFEGDLLVLCQC
AWQDWPLTQVTFYRDGSALGPPGPNREFSITVVKADSGHYHCSGIFQSP
GPGIPEVASVVAITVQELFPAPILRAVPSAEQAGSPMTLSCQTKLPLQR
SAARLLFSFYKDGRIVQSRLGSSEFQIPTASEDHGSYWC
EAATEDNQVW
KQSPQLEIRVQGASSSAAPTLNPA
PKSAA
PQTAPEEEAPGPLPPPP
TPS
SEDPGFSSPLGMPDPHLYHQMG
LLL
KHM
QDV
RVL
LGH
LL
MEL
REL
SGHRK
PGTTKATAE

Black = intracellular, Red = Transmembrane, Blue = Extracellular

Ly1464 has 358 amino acids and 3 Transmembrane Domains
Transmembrane Domain 1: 3 - 24 Score: 1.5484
Transmembrane Domain 2: 71 - 92 Score: 1.3009
Transmembrane Domain 3: 158 - 179 Score: 1.3027

FIG. 11



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Ly 1464 MHC class binding peptides (SEQ ID NOS: 10,599-10,819)

Ly1464 A1 binding peptides

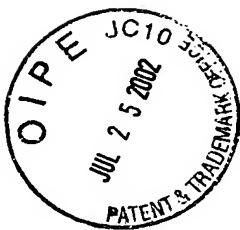
RANKING	SEQUENCE	STARTING POSITION	THEORETICAL SCORE
1	ATEDNQVWK	243	90
2	ASEDHSGSY	230	67.5
3	FSEPFHLIV	67	67.5
4	LTDAREAGF	52	25
5	SSEDPGFSS	300	6.75
6	ELFPAPILR	167	5
7	SSEFQIPTA	222	2.7
8	MPDPHLVHQ	312	2.5
9	LMBLRELSC	339	2.25
10	HTEDDLTDA	47	2.25
11	CTESESSCHT	40	2.25
12	ALGPPGPNR	118	2
13	LGMPDPHLV	310	1.25
14	CVLMAWALY	5	1
15	KADSGHYHC	135	1
16	LRELSGHRK	342	0.9
17	QLEIRVQGA	255	0.9
18	WCEAAATEDN	239	0.9
19	SAEPQAGSP	179	0.9
20	AREAGFQVK	55	0.9

Ly1464 HLA A2 binding peptides

RANKING	SEQUENCE	STARTING POSITION	THEORETICAL SCORE
1	YLSLGVLWV	13	4047
2	LLLKHMQDV	323	1006
3	VLMANALYL	6	739
4	VLWVAQMLL	18	301.4
5	MLLAASFET	24	271.9
6	ILQGPAAKEPV	81	118.2
7	LLGHILLMEL	334	83.53
8	LLAASFETL	25	33.81
9	WQDWPLTQV	102	29.84
10	YTFSEPFHL	65	29.29
11	LIVSYDWLI	73	18.29
12	KLPLQRSAA	195	17.39
13	WALYLSLGV	10	16.44
14	CQAWQDWPL	99	16.24
15	GIPETASVV	153	16.08
16	QVWKQSPQL	248	15.51
17	ALYLSSLGVL	11	8.38
18	QMGLLLKHM	320	8.252
19	VVAITVQEL	160	7.309
20	GVLWVAQML	17	6.916

Ly1464 A3 binding peptides

RANKING	SEQUENCE	STARTING POSITION	THEORETICAL SCORE
1	WLIQCGFAK	79	30
2	ELFPAPILR	167	18
3	ALGPPGPNR	118	9
4	VLWVAQMLL	18	6
5	VLMANALYL	6	5.4
6	LLKHMQDV	324	4
7	KLGCVLMAW	2	2.7
8	PMTLSQTK	187	2
9	LLGHILLMEL	334	1.8
10	GMMPDPHLVH	311	1.8
11	PLTQVTFYR	106	1.8
12	LLAASFETL	25	1.8
13	HLYHQMGLL	316	1.35



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14	ALYLSLGVL	11	1.35
15	YLSLGVLWV	13	1.2
16	ATEDNQVWK	243	1
17	HMQDVRVLL	327	0.9
18	HLIVSYDWL	72	0.9
19	KAYTPSEPF	63	0.9
20	KQSPQLEIR	251	0.81

Ly1464 All binding peptides

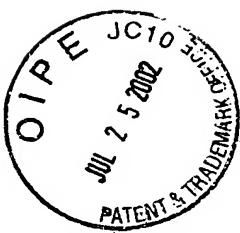
RANKING	SEQUENCE	STARTING POSITION	THEORETICAL SCORE
1	ATEDNQVWK	243	1
2	WLILQGPAK	79	0.6
3	KQSPQLEIR	251	0.36
4	CQTKLPLQR	192	0.24
5	RVLLGHLLM	332	0.18
6	PTLNPAPOK	270	0.15
7	ELFPAPILR	167	0.096
8	ARLLFSFYK	203	0.09
9	GVLWVAQML	17	0.09
10	LLKHMQDVR	324	0.08
11	ALGPPGPNR	118	0.08
12	GHRKPGTTK	347	0.06
13	RVQGASSSA	259	0.06
14	LPLQRSAAR	196	0.06
15	EFSITVVQK	127	0.06
16	YTFSEPPFHL	65	0.06
17	ITVQELPPA	163	0.045
18	YHQMGLLLK	318	0.04
19	QVWKQSPQL	248	0.04
20	LFSFYKDGR	206	0.04

Ly1464 A24 binding peptides

RANKING	SEQUENCE	STARTING POSITION	THEORETICAL SCORE
1	LYHQMGLL	317	200
2	VPEGDILLVL	89	30
3	TFYRDGSAL	111	20
4	GFOVKAYTF	59	15
5	KPVFEGDIL	87	12
6	HMQDVRVLL	327	10.08
7	GVLWVAQML	17	10.08
8	LYLSLGVLW	12	9
9	IFQSPGPGI	146	7.5
10	APEEAPGPL	285	7.2
11	TFSEPFHLL	66	7.2
12	HLLMELREL	337	6.6
13	MTLSCQTKL	188	6.6
14	VLMANALYL	6	6
15	HLIVSYDWL	72	6
16	GCVLMAWAL	4	6
17	LLGHLLMEL	334	5.28
18	VVAITVQEL	160	5.28
19	MAWALYLSL	8	4.8
20	DVRVLLGHL	330	4.8

Ly1464 A68 binding peptides

RANKING	SEQUENCE	STARTING POSITION	THEORETICAL SCORE
1	ELFPAPILR	167	45
2	ATEDNQVWK	243	30
3	ELRELSGHR	341	22.5
4	DVRVLLGHL	330	18
5	ALGPPGPNR	118	15
6	LPLQRSAAR	196	10
7	ETLQCEGPV	31	9
8	RVLLGHLLM	332	8
9	VVAITVQEL	160	8
10	WVAQMLLAA	20	8



11	GVLWVAQML	17	8
12	KQSPOLEIR	251	7.5
13	PTLNPAQPK	270	6
14	AVPSAEQPA	176	6
15	ETASVVAIT	156	6
16	VVQKADSGH	132	6
17	WLILQGPAK	79	6
18	LLKHMODVR	324	5
19	CQTKLPLQR	192	5
20	RVQGASSA	259	4

Ly1464 B7 binding peptides

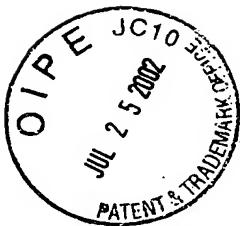
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1	DVRVLLGHL	330	200
2	KPVFEGDLL	87	80
3	APEEAPGPL	285	72
4	LQSAARLL	198	40
5	QVWKQSPQL	248	20
6	VVAITVQEL	160	20
7	IVSYDWLIL	74	20
8	GVLWVAQML	17	20
9	VLMAWALYL	6	12
10	MAWALYLSL	8	12
11	ALYLSLGVL	11	12
12	HMQDVRVLL	327	6
13	APGTAAPEEA	281	6
14	SPMTLSCQT	186	6
15	DAREAGFQV	54	6
16	RVLLGHLLM	332	5
17	HLLMELREL	337	4
18	LLGHLLMEL	334	4
19	VLMVAQMLL	18	4
20	HLYHQMGLL	316	4

Ly1464 B8 binding peptides

RANKING	SEQUENCE	STARTING POSITION	THEORETICAL SCORE
1	DVRVLLGHL	330	8
2	DAREAGFQV	54	7.2
3	LQSAARLL	198	1.2
4	PSFYIDGRI	207	1
5	GCVLMWAAL	4	0.8
6	MAWALYLSL	8	0.8
7	LLGHLLMEL	334	0.4
8	HLYHQMGLL	316	0.4
9	VLMAWALYL	6	0.4
10	AARLLPSFY	202	0.4
11	APILRAVPS	171	0.4
12	ALYSLGLV	11	0.4
13	HLYSYDWL	72	0.4
14	LLAASPFETL	25	0.4
15	VLMVAQMLL	18	0.4
16	HMQDVRVLL	327	0.3
17	APEEAPGPL	285	0.24
18	LSGRRKPGT	345	0.2
19	GVLWVAQML	17	0.2
20	SSSAAPPTL	264	0.2

Ly1464 B27 binding peptides

RANKING	SEQUENCE	STARTING POSITION	THEORETICAL SCORE
1	LRELSGHRK	342	2000
2	VRVLLGHLL	331	2000
3	ARLLPSFYK	203	2000
4	AREAGFQVK	55	2000
5	QRSAARLLF	199	1000



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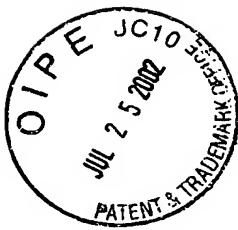
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7	NREFSITVV	125	600
8	KQSPOLEIR	251	300
9	HRKPGTTKA	348	200
10	IRVQGASSS	258	200
11	CQAWQDWPL	99	200
12	LRCQAWQDW	97	200
13	HLYHQMGLL	316	150
14	ALYLSLGVL	11	150
15	VLVVAQMILL	18	150
16	CQTKLPLQR	192	100
17	VQKADSGHY	133	100
18	LQGPAKPVF	82	100
19	AQMLLAASF	22	100
20	KAYTFSEPF	63	75

Ly1464 B35 binding peptides

RANKING	SEQUENCE	STARTING POSITION	THEORETICAL SCORE
1	KPVFEGDLL	87	60
2	WPLTQVTFY	105	40
3	EPFHLIVSY	69	40
4	TPSSEDPGF	298	30
5	GPPGPNRFP	120	20
6	AARLLFSFY	202	18
7	QSRGLSSEF	217	15
8	APEEAPGPL	285	12
9	VQKADSGHY	133	9
10	ASEDHSGSY	230	6
11	KAYTFSEPF	63	6
12	EAGFQVKAY	57	6
13	SSSAAPPTL	264	5
14	LSCQTKLPL	190	5
15	SSCHTEDDL	44	5
16	AATEDNQVW	242	4.5
17	KPGTTKATA	350	4
18	RVLLGHLLM	332	4
19	FPAPILRAV	169	4
20	DAREAGFQV	54	3.6

Ly1464 B44 binding peptides

RANKING	SEQUENCE	STARTING POSITION	THEORETICAL SCORE
1	LEIRVQGAS	256	30
2	WPLTQVTFY	105	27
3	SEDHSGSYW	231	24
4	REAGFQVKAY	56	18
5	EAGFQVKAY	57	13.5
6	LGMPDPHLY	310	12
7	SEFQIPTAS	223	12
8	AEPQAGSPM	180	12
9	QELFPAPIL	166	12
10	SEPFHLIVS	68	12
11	SAARLLFSF	201	9
12	VAITVQELF	161	7.5
13	ASEDHSGSY	230	6
14	AARLLFSFY	202	6
15	DDLTDAREA	50	4.5
16	FSITVVQKA	128	3.375
17	EPFHLIVSY	69	3
18	AQMLLAASF	22	3
19	TEDNQVWKQ	244	1.8
20	CEGPVCTSE	35	1.8



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ANALYSIS RESULTS OF THE PROGRAM TSITES.

.....

These are the results of the analysis of the file --> LY1464-1.TXT

Beginning with residue: 1 and ending with residue: 359

AMPHI Window size: 11

A - AMPHI mid points of blocks.

R - Residues matching the Rothbard/Taylor motif.

D - Residues matching the IAd motif.

d - Residues matching the IEd motif.

SEQ ID NO:
10,548

5 10 15 20 25 30 35 40 45 50 55 60 65 70 75
MKGCVLMAWALYLSGVLVWAQMILLAASFETLQCEGPVCTEESCHTEDDLTAREA
GFQVKAYTFSEPFHLIV

.....AAAAAAA...

.....RRRR.....RRRR.....RRRR.....RRRR

.....DDDDDD.....

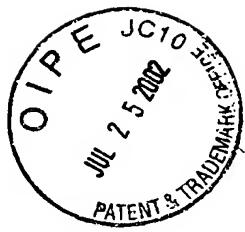
80 85 90 95 100 105 110 115 120 125 130 135 140 145 150
SYDWLILQGPAKPVFEGDLVLRCQAWQDWPLTQVTFYRDGSALGPPGNREFSITVVQ
KADSGHYHCSGIFQSP

.....AA.....AAAAAAA.....AAAAAAA

R.....RRRR..

.....

155 160 165 170 175 180 185 190 195 200 205 210 215 220 225
GPGIPETASVVAITVQELFPAPILRAVPSAEPQAGSPMTLSCQTKLPLQRSAARLLFSFYK
DGRIVQSRGLSSEF
AAAAAAA.....AAAAAAA.....
.....RRRR.....RRRRR.....RRRRR.....RRRR.....
.....DDDDDD.....DDDDDD.....DDDDDD.....DDDDDD..

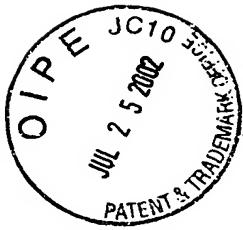


18/52

230 235 240 245 250 255 260 265 270 275 280 285 290 295 300
QIPTASEDHGSYWCEAATEDNQVWKQSPQLEIRVQGASSSAAPTLNPAPQKSAAPG
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.....AAAAA.....
.....RRRRR.....RRRRR.....
.....DDDDDDDDDD.....
.....

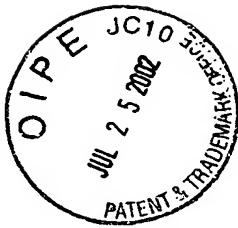
305 310 315 320 325 330 335 340 345 350 355 360 365 370 375
SEDPGFSSPLGMPDPHLYHQMGLLLKHMQDVRVLLGHLLMELRELSGHRKPGTTKATA
E
.....AAA.....AAAAAAA.....AAAAAAA.....
.....RRRR..RRRRR.....RRRRRRRRR.....RRRR....
.....DDDDDD.....
.....



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Table 4. Immunogenic portions of Ly1464 (SEQUENCES 1D,820-1D,842)

MKLGCVLMAWALYLSLGVLWVAQMILLAASF
LGVLWVAQMILLAASFETLQCEGPVCTEES
ETLQCEGPVCTEESSCHTEDDLTDAREAGF
CHTRDDLTDAEAGFQVKAYTFSEPFHLIV
QVKAYTFSEPFHLIVSYDWLILQGPAKPVF
SYDWLILQGPAKPVFEGDLLVLRQCQAWQDW
EGDLLVLRQCQAWQDWPLTOVTFYRDGSALG
PLTQVTFYRDGSALGPPGPNRPSITVVQX
PPGPNRPSITVVQXQADSGHYHCSGIFQSP
ADSGHYHCSGIFQSPGPGPETASVVVATV
GPGIPETASVVVATVQELFPAPILRAVPSA
QELFPAPILRAVPSAEPQAGSPMTLSCQTK
EPQAGSPMTLSCQTKLPLQRSAARLLPSFY
LPLQRSAARLLPSFYKDGRIVQSRGLSSEF
KDGRIVQSRGLSSEFQIPTASEDHGSYWC
QIPTASEDHGSYWCQAAATEDNQVWKQSPQ
EAATEDNQVWKQSPQLEIRVQGASSSAAPP
LEIRVQGASSSAAPP TLNPAPQKSAAPGTA
TLNPAPQKSAAPGTAPEAPGPLPPPPTPS
PEEAPGPLPPPPTPSSEDPGFSSPLGMPDP
SEDPGFSSPLGMPDPHLYHQMGLLLKEMQD
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VRVLLGHLLMELRELSGHRKPGTTKATAE



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Ra12-LY1464 profile

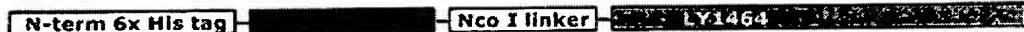
CORIXA CORPORATION
Antigen Discovery

LY1464 and recombinant Ra12-LY1464

Researcher: Alex Gaiger, Aijun Wang, Jonathan Clapper
Reference: cloning bk813 pg150, 151, 154-157; expression bk966 pg2-3

Description: LY1464 is an antigen discovered by Lymphoma program. The full-length sequence was cloned through PCR amplification of normal tissue cDNA known to express the gene. The gene was cloned directly into the pCRX2 vector as an N-terminal Ra12 fusion, **Ra12-LY1464**, using restriction enzymes Nco I and Xho I, and the sequence was subsequently confirmed. The optimal protein expression conditions were determined by mini-induction screening.

Protein Diagram of Ra12-LY1464



Cloning Strategy:

Tumor and normal tissue derived cDNAs (from Alex Gaiger) were each used separately as templates in PCR amplification reactions with two primers (LY1464-sense and LY1464-antisense) flanking the 5' and 3' ends of the gene LY1464. As shown below, the primers contained short 5' restriction enzyme recognition sequences. The PCR products were separated on agarose gel and the DNA band of ~1080bp was gel purified. This 'insert' was digested using restriction enzymes Nco I and Xho I and ligated to pCRX2, which was linearized with the same two restriction enzymes and then dephosphorylated. The vector and insert were combined in equi-molar ratios with DNA ligase to create a completed plasmid construct pCRX2 Ra12-LY1464. This ligation mixture was used to transform competent E. coli Novablue cells. Ten individual colonies from both tumor cDNA derived and normal cDNA derived construct were picked for DNA miniprep. Miniprep samples were screened for insert through restriction enzyme digestion (Nco I, Xho I) and five positive samples were sent for DNA sequencing. Miniprep clone #4 (Corixa seq ID#90522) was confirmed and used for expression of recombinant Ra12-LY1464 in E. coli.

Cloning Primers:

LY1464-sense
 5' - CGTCCATGGACatgaagctgggtgtgtcc - 3' (SEQ ID NO:10,843)
 prime 21bp 57%GC 56C Tm
 full length 32bp 59%GC 68C Tm

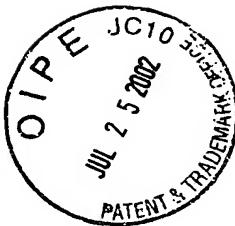
LY1464-antisense
 5' - CCTTCTCGAGctattcagcagtgcgtttgtggcc - 3' (SEQ ID NO:10,844)
 prime 25bp 48%GC 58C Tm
 full length 35bp 51%GC 67C Tm

Protein Expression:

Various E. coli strain/culture conditions were screened for optimal expression conditions for recombinant protein expression. Briefly, the expression construct was used to transform different expression hosts, and then mini-induction cultures were screened at varied culture temperature, culture media and/or IPTG concentration. The optimal expression condition was determined by evaluating the results of SDS-PAGE and western blot.

For Ra12-LY1464, The most optimal expression condition is pCRX2 Ra12-LY1464 in Tuner (DE3) CodonPlus-RP grown in 2xYS media at 37°C induced with 1.0mM IPTG at 25°C (room temp) for 3hr.

FIG. 15



Ra12-LY1464 profile

CORIXA CORPORATION
Antigen Discovery

DNA/Protein Sequence:

LY1464 (DNA) 1080bp (SEQ ID NO: 10, 1/45)

atgaagctgggctgtgtccatggcctggcccttaccccccgggtgggtgtctctgggtggcccaagat
gtcaactggctggccagggtttggagacgtgtggggacactgtgcactgaggagagcagctgcacca
cggaggatgacttgcgtactgtcaaggaaagctgggtttccaggtaaggccactacacttcaggtaacccttc
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gtcaactgtcaatag

Ra12-LY1464 (DNA) 1500bp (SEQ ID NO: 10, 4/67)

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ggc
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atgtgtccatgtactgtgtatccatccaggatccatccatcaggatccatccatcaggatccatccatcaggatcc
gcgtgcggc
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gtcaatag

Ra12-LY1464 (protein) (SEQ ID NO: 10, 4/68)

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LGCVLMAWALYSLGVLNVAQMLLAASFETLQCEGPVCTEESSCHTEDDLTDAREAGFQVKAYTFSEPFHL
IVSYDWLILQGPAKPVFEGDLLVLRQCAWDNPLTQVTFYRDGSALGPPGPNRFSITVVQKADSDGHYHCS
GIFQSPGPGIPETASVVAITVQELFPAPILRAVPSAEPQAGSPMTLSCQTKLPLQRSAARLLFSFYKDGR
VQSRGLSSEFQIPTASEDHSGSYWCEAATEDNQVWKQSPQLEIRVQGASSSAAPTLNPAPQKSAAPGTAP
EEAPGPLPPPTPSSEDPGFSPLGMPDPHLYHQMGLLLKHMQDVRLVLLGHLLMELRELSGHRKPGTTKAT
AE.

Protein Info:

Ra12.LY1464

Molecular Weight 53010.15 Daltons

499 Amino Acids

29 Strongly Basic (+) Amino Acids (K,R)

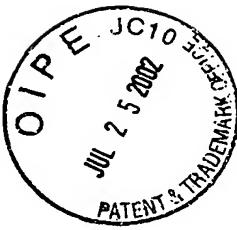
46 Strongly Acidic (-) Amino Acids (D,E)

174 Hydrophobic Amino Acids (A,I,L,F,W,V)

128 Polar Amino Acids (N,C,Q,S,T,Y)

5.663 Isoelectric Point

-14.119 Charge at PH 7.0

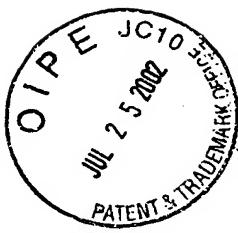


22/52

1484

LyM48. DNA Sequence (SEQ ID NO: 10, 846)

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 121 ctgcccccttc tcttgcacac atctctctgt tcacccagaa getgggtggag aagctgtaca
 181 gtgggtatgtt ctggccagac cccagccata tcctccctt ctcctggag cacatcatgg
 241 tggtcattgt aactgtctt ttcataaggg aactgtctt cagccacttta tacagcagg
 301 taaataaagt cattttttat tgcctatcca aeccccagca gtcctctcc gaatgcctcg
 361 gcttctccgc cattctggc ttctcgccgg agactgggaa tgggtctttt gccacccata
 421 attcacacat cagttcttc ctgtgtcttc tgcatgttgc ttgtgtactc aatgagagaa
 481 gttacccaga aggatttggg ttggagccca agcttataat gtctacttat catcaagtct
 541 tcctttccccc aaatgttggg agtggaaaggaa aaagagaaggat ttaccatgtt ttgagtgtat
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 1261 atgaaactgtac actggggggat gctggggggc agccggacca ggtgggggggtt gactgcaccc
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 1741 ttccatgttgc ttacaaacatc gtcgttggat gggccatctgg aatgttcttgc tttttccaaat
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 1861 ctgacaggat catgttgcgtt aagtggcaga aaggggacat cagcaatttt ggttgcacca
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23/52

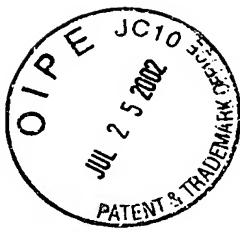
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 4141 cttactggaa attattgtat tgtcttatt ttattaaagc aactatgtt t

Ly1484. Protein sequence (long) (SEQ ID NO: 10,847)

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 HCLLNLNERSYPEPGPLEPKPRMSTYHQVPLSPNEDVKEKREDLPSLSDV
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 DPECKTEDFVSCIEINYRRRGQELYASLYKDHVQRRKCGNIKAANAWARIQ
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 LHSEDPLELCSRERQVILQELLDKEKVTQKFSLVIVQGHLVSEGVLFFGHQ
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 SLKGKATSEDTLNLRYPGSDRIMIQLQWQKRDISNPEYLMYLNTAAGR
 NDYMQYPVPPWVLADYTSETLNLANPKIFRDLSPKPMGAQTKERKLKPIQR
 FKEVEKTEGDMTVQCHYYTHYSSAIIVASYLVRMPPFTQAFCALQGGSFD
 VADRMFHSVKSTWESASRENMSDVRRELTPPEFFYLPEFLNCNGVEFGCMQ
 DGTVLGDVQLPPWADGDPRKFISLHRKALESDFVSANLHHWIDLIFGYKQ
 QGPAAVDAVNIFHPYFYGDRMDLSSITDPLIKSTILGFVSNFGQVPKQLF
 TKPHPARTAAGKPLPGKDVSPLPGHQPPFFYSLQSLRPSQVTVKDMY
 LPSLGSES PKGAIGHIVSTEKTILAVERNKVLPPLNRTPSWGFDDFSC
 CLGSYGSQDKVLMTFENLAAWGRCLCAVCPSPPTIVTSGTSTVVCWELSM
 TKGRPRGLRLRQALYGHQAVTCLAAVSFTPSLLVSGSQDCTCILWLDLHL
 THVTRLPAHREGISAITISDVSGTIVSCAGAHLSLWNVNGQPLASITTAW
 GPEGAITCCCLMEGPAWDTSQIIITGSQDGMRVWKTEDVKMSVPGRPAG
 EEPPLAQPPSPRGHKWEKNLALSRELDVSIALTGKPSKTSPAVTALAVSRN
 HTKLLVGDERGRIFCWSADG

Ly1484. Protein sequence (short) (SEQ ID NO: 10,848)

MLQKWQKRDISNPEYLMYLNTAAGR CNDYMQYPVPPWVLADYTSETLN
 ANPKIFRDLSPKPMGAQTKERKLKF IQRFKEVEKTEGDMTVQCHYYTHYSS
 AIIIVASYLVRMPPFTQAFCALQGGSFDVADRMFHSVKSTWESASRENMSD
 VRELTPEFFYLPEFLNCNGVEFGCMQDGTVLGDVQLPPWADGDPRKFIS
 LHRKALESDFVSANLHHWIDLIFGYKQGPAAVDAVNIFHPYFYGDRMDL
 SSITDPLIKSTILGFVSNPGQVPKQLPTKPHPARTAAGKPLPGKDVSPTV
 SLPGHPQPPFFYSLQSLRPSQVTVKDMYLFSLGSESP KGAIGHIVSTEKT
 ILAVERNKVLPPLNRTPSWGFDDPSCCLGSYGSQDKVLMTFENLAAWGR
 CLCAVCPSPPTIVTSGTSTVVCWELSMTKGRPRGLRLRQALYGHQAVTC
 LAASVTPSLLVSGSQDCTCILWLDLHLTHVTRLPAHREGISAITISDVSG
 TIVSCAGAHL SLWNVNGQPLASITTAW GPEGAITCCCLMEGPAWDT
 SQIIITGSQDGMRVWKTEDVKMSVPGRPAG EEPPLAQPPSPRGHKWE
 KNLALSRELDVSIALTGKPSKTSPAVTALAVSRNHTKLLVGDERGRIFC
 WSADG



a. TMpred Report for Ly1484 Long

Date:

RDFQSEVLLSAMELHMTSGGDAAMFRDGKEPQPSAEAAAAPSLANISCF
TQKLVEKLYSGMFSADPRHILLFILEHIMVIETASSQRDTVLSTLYSSL
NKVILYCLSKPQQSLSECLGLLSILGFLQEEHWDVVFATYNSNISPLLCLM
HCLLLLNERSYPEGFGLEPKPRMSTYHQVFLSPNEDVKEKREDLPSLSDV
QENIQKTVQTLWQQLVAQROQTLDEADFKIDLSVKPGEREVKIEEVTPW
ETMLKAWQHYLASKEKKSLASRSNVAAHHSKTVLWQGSLSLSAMKLMPGRQAK
DPECKTEDFTVSCIEENRRRGQELYASLYKDHVQRRKCGNIAANAWARIQ
EQLFGELGLWQSQEETKPCSPDWLREYPARMRKRIKRLSPLEALSSGR
HKESEDQDKNDHISQTNAENQDELTREAEGEPEDEVGVDCTQLTFFPALHRS
LESEDFLELCRERQVILQELLDKEKVQKFLSLVIVQGLVSEGVLLPGHQ
HFYICENFTLSPTGDVYCTRCLSNSIDSPFIFNLCSDKRSTDHYSCQCHS
YADMRELQRQARFLLQDIALEIFFHENGYSKFLVFYNNDRSKAFKSFCSFQCP
SLKGKATSEDTLNLRYPGSDRIMLQKWNQKRDISNPEYLMYNTAAGRTC
NDYMQYPVFPWVLADYTSETLNLANPKIFRDLSKPMGAQTKERKLKPIQRF
FKEVEKTEGDMTVQCHYTHYSSAIIVASYLVRMPPFTQAFCALQGGSF
VADRMFHHSVKTWSASRNMDSVDRLETFYPLFNTCNGVEFGCMQ
DGTVLGVDQVLFWADGDPRKFISLHRAKALESDFVSAHLHWIDLIFGYKQ
QGPAAVDAVNIFHPYFYGDRMDLSSITDPLIKSTILGFVSNFGQVPKQLF
TKPHPARTAAGKPLPGKDVSPTVSLPGHPQPFYSLQSLRPSQVTVKDMY
LPSLGSESPKGAIIGHIVSTEKTILAVERNKVLPLWNRTFSWGFDDFSC
CLGSYGSKDKVLMTFENLAANGRCLCAVCPSPPTIIVTSGTSTVVCVWELSM
TKGRPRGLRLRQALYGETQAVTCLAASVTFSSLVSGSQDCTCILWLDLDDH
TEVTRLPAHREGISAITISDVSGTIVSCAGAHLISLWNVNGQPLASITTA
GPEGAITCCCLMEGPAWDTSQIIITGSQDGVMVRWKTEDVKMSPVGRPAG
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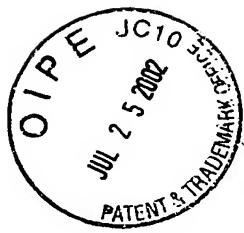
Black = intracellular, Red = Transmembrane, Blue = Extracellular

Lyl1484 Long has 1269 amino acids and 5 Transmembrane Domains
Transmembrane Domain 1: 63 - 84 Score: 1.36675
Transmembrane Domain 2: 118 - 139 Score: 1.38695
Transmembrane Domain 3: 480 - 501 Score: 1.36185
Transmembrane Domain 4: 562 - 583 Score: 1.31785
Transmembrane Domain 5: 725 - 746 Score: 1.3521

b. TMpred Report for Ly1484 (short)

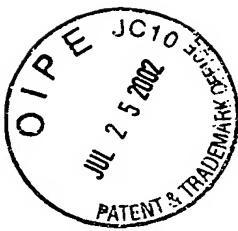
MLQKWKQRDISNFEYMLNTAAGRTCNDYMQYPVFPWVLADYTSETLNL
ANPKIPRDLSKPMGAQTKERKLFIQRFKEVKTGDMTVQCHYTHYSS
AIIVASYLVRMPPFTQAFCALQGGSFVDARMFBSVKSTWESASRENMSD
VRELTPEFFYLPFELTNCGVFGCMQDGTVLGVDQLPPWADGDPRKFIS
LERKALESDPVSANLHEWIDLIFGYKQQGPAAVDAVNIFHPYFYGDRMDL
SSITDPLIKSTILGFVSNFGQVPKQLFTKPHPARTAAKGKPLPGKDVTSPV
SLPGHPQPFYSLQSLRPSQVTVKDMYFLSGSESPKGAIIGHIVSTEKTI
LAVERNKVLLPPLNNRTFWSWGFDDFSCCLGSYGSKDVKLMTFENLAAWGRC
LCAVCPSPTTIVTGTSTVVCVWELSMTKGRPRGLRLRQALYGHQAVTC
LAASVTPSLLVSGSQDCTCILWDLDLHVTRLPAHREGISAITISDVSG
TIVSCAGAHLSLWNVNGQPLASITTAWGPEGAITCCCLMEGPAWDTSQII
ITGSQDGVMRVWKTEDVKMSPVGRPAGEEPLAQOPPSRGRHKWEKNLALSR
ELDVSIALTGKPSKTSPAVTALAVSRNHTKLLVGDERGRIFCWSADG (SEQ ID NO: 10,848)

Black = intracellular, Red = Transmembrane, Blue = Extracellular



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Ly1484 has 646 amino acids and 1 Transmembrane Domains
Transmembrane Domain 1: 102 - 123 Score: 1.3521



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Table 2a: Ly1484 long MHC class I binding peptides
(SEQID NOS: 10,849 - 10,908)

HLA A2:

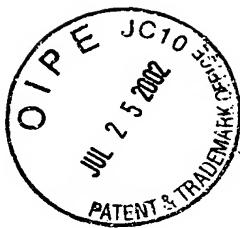
RANKING	SEQUENCE	STARTING POSITION	THEORETICAL SCORE
1	FLICLMHCL	145	836.3
2	YLPEFLTNC	783	818.9
3	KLYSGMPSA	57	742.3
4	FILEHIMVW	73	629.3
5	TLYSSLNKVV	95	511.9
6	FLQERHMDVV	127	448
7	IILWDLDDHLT	1093	431.1
8	ALQGGGSFDV	743	403.4
9	MQYPVFPWV	654	400.9
10	ALYGMHTQAV	1063	222.6
11	YLVRMPPFT	730	188.5
12	CLMHCLLLL	148	181.8
13	GLLSILGFL	120	130
14	VIMTFENLA	1010	118.7
15	IILAVERNKV	973	118.2
16	YLASEKKSL	260	98.27
17	ELTPPEFFYL	776	97.11
18	YLMYLMTAA	638	84.56
19	ILLFILEHI	70	73.96
20	LLQDIALEI	563	72.72

HLA A3

RANKING	SEQUENCE	STARTING POSITION	THEORETICAL SCORE
1	KLMPGGRQAK	292	135
2	VLLPPPLWNR	981	60.75
3	CLGSYGSQDK	1001	60
4	KVILYCLSK	102	54
5	CVWELSMTK	1044	30
6	LLFGHQHFPY	495	30
7	PLWEETMLK	247	30
8	FLSPNEDVK	180	30
9	SLYKDHVQR	326	20
10	FLVFYNNDR	580	18
11	KLYSGMPSA	57	13.5
12	GLRLRQALY	1057	12
13	NLANPKIFR	672	12
14	RVWKTEDVK	1183	10
15	QVPKQLFTK	694	9
16	RMPPFTQAF	733	9
17	KLXPIQRPK	694	9
18	RIMLQKQKQK	622	9
19	VILOELLDK	465	9
20	IMLQKQKQR	623	6

HLA A24

RANKING	SEQUENCE	STARTING POSITION	THEORETICAL SCORE
1	OYPVFPWVL	655	300
2	FYICENFTL	502	300
3	TYNSNISPL	138	300
4	NYRRRGQEL	315	264
5	DYTSETLNL	665	200
6	SYLVRMPPF	729	150
7	RYPGSDRIM	616	75
8	RPLLQDIAL	561	60
9	LYSSLNKKVI	96	60
10	YTHYSSAI	717	50
11	PFPALHESL	443	36
12	NFGQVPKQL	891	28
13	SYGSDKVLM	1004	25
14	GFDDDFSCCL	994	24
15	EFFYLPEFL	780	24
16	YFYGDRKMDL	865	20
17	SPCSFQPSL	594	20
18	RGLRLRQAL	1056	17.28
19	RGQELYASL	319	17.28
20	KNLALSREL	1217	15.84



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CID1096 Table 2b. Ly1484 short MHC class I binding peptides
(SEQ ID NOs: 10,901 - 10,968)

A2

RANKING	SEQUENCE	STARTING POSITION	THEORETICAL SCORE
1	YLPEFLTNC	160	818.9
2	ILWDLQMLT	470	431.1
3	ALOGGSDV	120	403.4
4	NOYPVFPNV	31	400.9
5	ALYGHQTAQAV	440	222.6
6	YLVRMPPPT	107	168.5
7	VLMTFENIL	387	118.7
8	ILAVERNKV	350	118.2
9	ELTPEFFYL	153	97.11
10	YLMYLNTAA	15	84.56
11	VLADYTSSET	39	51.94
12	RKPHSVIEST	131	45.8
13	SNFEYLAYL	11	26.76
14	KVLMTFENL	386	22.54
15	LLPPLMVRT	359	21.54
16	QLFTKQPHPA	275	18.38
17	GAHLSIANNV	507	16.66
18	WILDHLTHV	472	16.5
19	FISLHRAKAL	198	13.51
20	CILWDLQNL	469	12.25

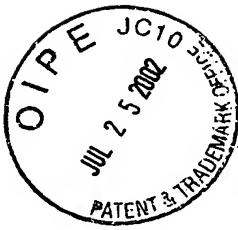
HLA A3

RANKING	SEQUENCE	STARTING POSITION	THEORETICAL SCORE
1	VLLPPLANNR	358	60.75
2	CLGSYGSOK	378	60
3	CWELSMITK	421	30
4	GLRLRQALY	434	12
5	HLANPKIPR	49	12
6	RVWKTEDVK	560	10
7	QVPKQQLPTK	271	9
8	RMPPTQAF	110	9
9	KLKPIORFK	71	9
10	TILGFVSNF	261	4.05
11	SLEGHPOQPF	301	3
12	WIDLIFPGYK	218	2.7
13	NLHHWIDLII	214	2.7
14	YMQYFVFFW	30	2.7
15	ELTPEFFYL	153	2.43
16	ALYGHQTAQAV	440	1.5
17	YLPEFLTNC	160	1.35
18	IIVASYLVR	102	1.2
19	DMTVQCHYY	87	1.2
20	QLPTKQPHPA	275	1

HLA A24

RANKING	SEQUENCE	STARTING POSITION	THEORETICAL SCORE
1	QYPVFPWVL	32	300
2	DYTSETLNL	42	200
3	SYLVRMPPF	106	150
4	YTHYSSAI	94	50
5	NPGQVPKQL	268	28
6	SYGSDIVLVM	381	25
7	GFDDYSSCL	371	24
8	EFFYLPEPL	157	24
9	YFYGDRMDL	242	20
10	RGLRLRQAL	433	17.28
11	IKRLALSREL	594	15.84
12	KVLMTFENL	386	14.4
13	TFSMGPDDOF	367	12
14	FYLPEPLTN	159	10.8
15	ANPKIPRDL	51	10.08
16	SPDVAADRME	125	10
17	KTSPAVTAL	614	9.6
18	KGRPRGLRL	429	9.6
19	RNKVLLPPL	355	9.6
	SYLMYLNTA	14	9

FIG. 20



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ANALYSIS RESULTS OF THE PROGRAM TSITES.

These are the results of the analysis of the file --> LY1484-1.TXT
Beginning with residue: 1 and ending with residue: 1270
AMPHI Window size: 11

- A - AMPHI mid points of blocks.
- R - Residues matching the Rothbard/Taylor motif.
- D - Residues matching the IAD motif.
- d - Residues matching the IED motif.

80 85 90 95 100 105 110 115 120 125 130 135 140 145 150
EHINVVVIETASSORDTVLSTLYSSLNKVILYCLSKPOQSLSECILGLISLIGFLCENHWDVFATYNSNISVFLCLM
.....AAAAAAA.....AAAAAAAAAAAAAAAAAAAAAAA.....
.....RRRRR.....RRRRR.....RRRRR.....RRRRR.....

155 160 165 170 175 180 185 190 195 200 205 210 215 220 225
HCLLILNERSYPEGPCLEPKPRMSTYHQVPLSPNEQDVKEKREDLPSLSDVQHENIQLKTVOQLMQQVLAQROQTLED
.....AAAAA.....AAAAA.....AAAAA.....RERER.....R

230 235 240 245 250 255 260 265 270 275 280 285 290 295 300
APKIDLSVKGPEREVKIEEVTPLWEETLKGAMONYLASEKKSLASRSRNVAHHSKVTLWSGSLLSAMKLNPGRQAK
.....AAAAAAA.....RRRRRRRRRRRRR.....RRRRR.....
RRR.....
d444.

305 310 315 320 325 330 335 340 345 350 355 360 365 370 375
DPECKTEDPVSCINYRRRCQ2LYASLYKDHVORRKCGHIIKARAHAWARIEQQLFCGELGLHSOG2ETKPCSPWELD
.....AAAAAA.....AAAAAA.....AAAAA.....AAAAA.....AAA
.....RRRR.....RRRR.....RRRR.....RRRR.....RRRR.....RRRR.....

380 385 390 395 400 405 410 415 420 425 430 435 440 445 450
WRECPARMRKRIRKRLSPLAESSGRHDXSDQHODHISQTMNAENQDELTURAECEPDEVGVDCITQLTYPFPAHES
.....AAAAAAA.....RRRR.....RRRRR.....AAAAA.....
.....DDDDDD.....DDDDDD.....
.....dddd.....

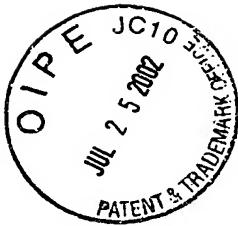
455 460 465 470 475 480 485 490 495 500 505 510 515 520 525
LHNSEDPFLCRLCRQVILQELLDKEKVTKQPKSLVIVOGHLVSEGVLILPGHCHFVTCNTLSPYGDVYCTRILCNSL
.....AAAAA.....RRRR.....RRRR.....RRRR.....RRRR.....AAAAA

530 535 540 545 550 555 560 565 570 575 580 585 590 595 600
ISDPPFIMLCSKDRSTHDYSCQHKSADHRELQRAPRLQDIALBIPPFHNGYSKFLVPMNDRSXKAFCSCFSCPQP
A. AAAAAA..... AAAAAAAAAA..... AAAAAA..... RRRRRRRRRRRRRR..... RRRR

605 610 615 620 625 630 635 640 645 650 655 660 665 670 675
SLKGKATSEDTLNLRRYPGSDRIMLQKMQKRDISHNFPEYLAVLNTRAGRTCDYMOYPVFPVNLADYTSTLNLAN
.....AAAAA.....AAA.....AAAAAAA.....
....RRRR.RRRR.....RRRRR.....RRRR.....RRRRRRRR...
DDDDDD...

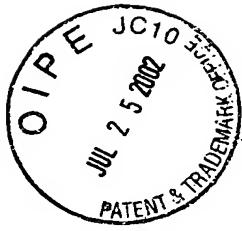
680 685 690 695 700 705 710 715 720 725 730 735 740 745 750
PKI PRDLKSKPQMAQTKERIKLKPFIQRFKEVKEPTEGDMVYQCHYYTHYSSAIIVASYLVRNPPPTQAPCALOGGSFD
AAAAAAAAAAAAA.....AAAAAAAAA.....AAAAA.....A
.RRRR.....RRRR.....RRRRR.RRRRR.....R

FIG. 21
Page 1 of 2



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FIG. 21
Page 2 of 2



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ANALYSIS RESULTS OF THE PROGRAM TSITES.

These are the results of the analysis of the file --> LY1484-2.TXT
Beginning with residue: 1 and ending with residue: 647
AMPHI Window size: 11

A - AMPHI mid points of blocks.
R - Residues matching the Rothbard/Taylor motif.
D - Residues matching the IAd motif.
d - Residues matching the IEd motif.

SEQ ID NO.
10,848

5 10 15 20 25 30 35 40 45 50 55 60 65 70 75
MLQKQKQKRDISNPEYLNLNTAAAGRTCDYQYVFPWVLAQTYSETLMLANPKIFRDLSKPHGAQTKERKLKPI
....AAA.....AAAAAAA.....RRRRR.....RRRR.....AAA.....RRR
.....d...

80 85 90 95 100 105 110 115 120 125 130 135 140 145 150
QRPKVEKTEGDMTVQCHYTHYSSAIIVASYLVRMPPQTQAPCALQGGSPDVADRMPHSVKSTWESASRENMSD
AAAAAAA.....AAA.....AAA.....AAA.....AAA.....AA.....AA
R.....RRRR.RRRR.....RRRRR.....RRRRR.....
.....

155 160 165 170 175 180 185 190 195 200 205 210 215 220 225
VRELTPPEFYLPPEFLTNCHGVEFGCMQDGTVLGDVQLPPWADGDPKPISTLHRKALESDPVSANLHRWIDLPGY
AAA.....AAAAA.....AAA.....AAA.....AAA.....AAA.....AAA.....AAA
....RRRRR.....RRRR.....RRRR.....RRRR.....RRRR.RRRR.....RRRRR.RR
.....

230 235 240 245 250 255 260 265 270 275 280 285 290 295 300
KQQGPAAVDAVNIFKPYPYCDRMDLSSITDPLIKSTILGPVSNPGOVPKQLPKPHPARTAAGKPLPGKDVTSPV
....AAAAAAA.....AAA.....AAA.....AAA.....AAA.....AAA.....AAA
....RRRR.....RRRR.....RRRR.....RRRR.....RRRR.....RRRR.....RRRR
.....DDDDDD.....DDDDDD.....DDDDDD.....DDDDDD.....DDDDDD
.....

305 310 315 320 325 330 335 340 345 350 355 360 365 370 375
SLPGHPOPPFYSLQSLRPSQVTKDMDYLFSLGSESPKGAIICHIVSTEKTILAVERNKVILLPLMNRTFGWGFDCP
AAA.....AAA.....AAA.....AAA.....AAA.....AAA.....AAA.....AAA
D.....RRRRR.....RRRR.....RRRR.....RRRR.....RRRR.....RRRR
.....DDDDDD.....DDDDDD.....DDDDDD.....DDDDDD.....DDDDDD
.....

380 385 390 395 400 405 410 415 420 425 430 435 440 445 450
SCCLGSYGSQDVKLMTFENLAAGRCLCAVCPSPPTIVTSGTSTVVCVMELSMTKGRPRGLRLRQALYGHTOAVTC
....AAAAAAA.....AAA.....AAA.....AAA.....AAA.....AAA.....AAA
....RRRR.....RRRR.....RRRR.....RRRR.....RRRR.....RRRR
.....DDDDDD.....DDDDDD.....DDDDDD.....DDDDDD.....DDDDDD
.....dd...

455 460 465 470 475 480 485 490 495 500 505 510 515 520 525
LAASVTPSLIVSGSQDCTCILWDLHDHLTHVTRLPAHREGISAITISDVSGTIVSCAGAHLSLMLVNGQPLASIT
....AAA.....AAA.....AAA.....AAA.....AAA.....AAA.....AAA
....RRRR.....RRRR.....RRRR.....RRRR.....RRRR.....RRRR
.....DDDDDD.....DDDDDD.....DDDDDD.....DDDDDD.....DDDDDD
.....

530 535 540 545 550 555 560 565 570 575 580 585 590 595 600
ANGPEGAITCCCLMECPANDTSQIIITGSQGMVRWVKTEDVQMSVPGRPAGESPLAQPPSPRGHOMENNLALSR
....AAA.....AAA.....AAA.....AAA.....AAA.....AAA.....AAA
....RRRR.....RRRR.....RRRR.....RRRR.....RRRR.....RRRR
D.....DDDDDD.....DDDDDD.....DDDDDD.....DDDDDD.....DDDDDD
.....

605 610 615 620 625 630 635 640 645 650 655 660 665 670 675
ELDVSIALTGKPSKTSPTAVTALAVSRNHTKLLVGDERGRIFCWSADG
.....RRRR.....RRRR.....RRRR
.....DDDDDD.....DDDDDD.....DDDDDD.....dd...
.....

Ly1456P LifeSeqGold Clone Distribution

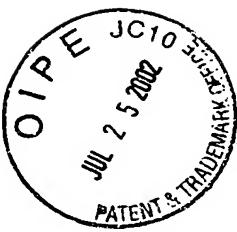
Ly1456P LifeSeq Gold Search

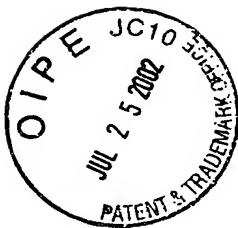
LifeSeq Template	E Value of hit	Length (bp)	Libraries Found in		Clone Abundance		ORFs * (>50aa)	TMpred **
			Total #	Hemic & Immune #	Total Clone Count	Hemic & Immune		
238330_1	0	1442	55	21	78	33	294bp 177bp 252bp 198bp	No No No No

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- * = Template sequence was searched for ORFs using MapDraw (4 potential ORFs identified).
- ** = Predicted ORFs were translated and were analyzed for potential TM regions using TMpred.

ORF#1 = 379>672 = 294bp = 98aa
 ORF#2 = 555>734 = 177bp = 59aa
 ORF#3 = 1037>1291 = 252bp = 84aa
 ORF#4 = 1074>1274 = 198bp = 66aa





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SEQ ID NO: 10,475

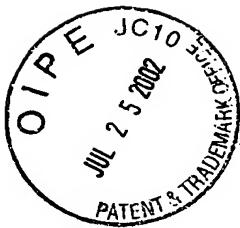
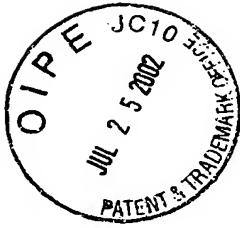
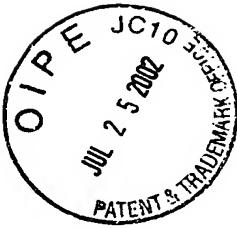


FIG. 24
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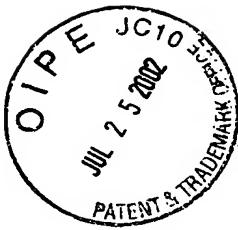


9721 tcttagttgtct gtatccccctt tcccttaatgt aaaaagtatc tcactaaccc ttcttcata
 9781 ttttttcttc cttactttct tetaatcact ttaggatatt agatgtctt ctccaaatgt
 9841 agaaatttgc aataatgtgc tttagccccac attacataa actttttctt ttgggggggt
 9901 agagtgtatt attatatca cagttaact atgtctgtc agggggtact ttcaagacac
 9961 catgaatttca acagcatctt cgaataagca tttttcttt ccaattttag acaagatttg
 10021 gaagtttaca aaccattaa taatatggct tcaatgttgc gcatgttct cactcactca
 10081 cacacacaca cacacaaaaa acatgttgc aacactttcc atatagtctt gctccccaaa
 10141 ggggtatgt tcgggttcagg ggacaccctg taagacaatg cgctgcattt aacccattt
 10201 tcaagccaaa gccaagaca tgaagacggc tcccacaggg tgcacaccctc cagcaagtga
 10261 atacatgtgt agcagcagag catgtctgtg gaagttggggg aaaaagcaga aaccaagtg
 10321 ggcggaaaattt tgcttattt gtattttca aatatgttgc tttttggact tacattagca
 10381 gcttagaaatgt aatgttgc tttttttact tcagaacggc attttttggaa ggatgttcatc
 10441 ccactgtttaa taaaatatac ggcggggcac agtggctcat gcttgaatc ccagcaattt
 10501 gagaggccga ggtggccaga tcactgttgc tcaaggatgtt gagaacagcc tggacaacat
 10561 ggccaaaccc tggcttctact aaaaatatac aaaaatgttgc gaggatgtt ggggtgcct
 10621 gtaatcccaag ctactttggg ggtctggggca ggaatcat ttaaaccagg gaggccgagg
 10681 ctggcgttaag ctgagatttc accatttgcac tccagcttgc gcaacaagag caaaactctg
 10741 tctcaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa
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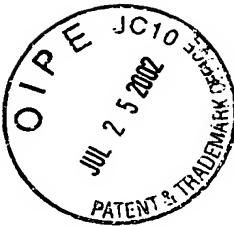
FIG. 24
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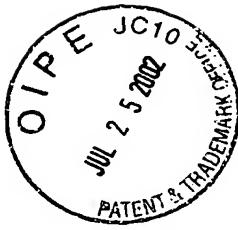
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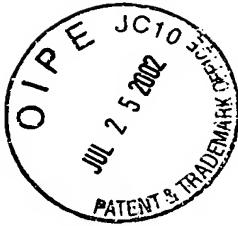


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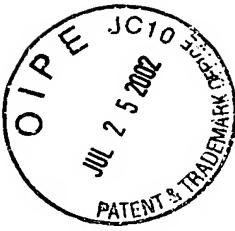
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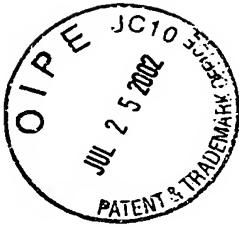


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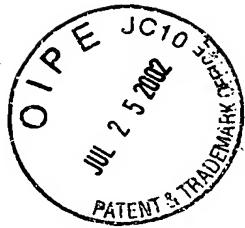
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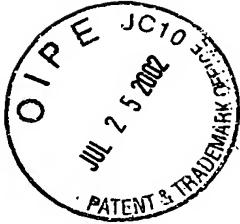
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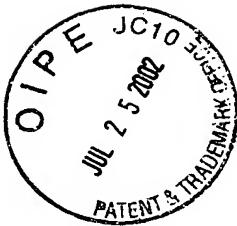
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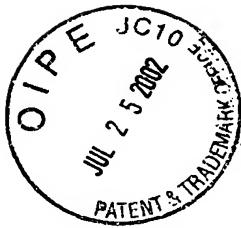
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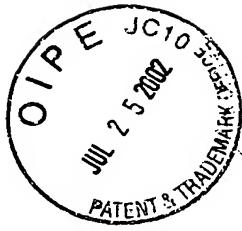
45/52

Ly1488 Protein Sequence (SEQID ND: 10, 965)

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Ly1488 DNA Sequence (mRNA) (SEQ ID NO: 10, 970)

11



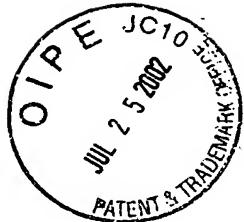
46/52

TMpred Report for Ly1488 (SEQ ID NO: 10,969)

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D S N G N S M L S N Q D A F R L W C L F N P L S E D K Y P L I M V P D E G D E G N H P S P E P V P S
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P Q L Q P S C L C Y P G S E B C K E K R G I I P L D A H C C V E V L P D R D G K R C M F C V K T A N
R T Y E M S A S D T R Q R Q E N T A A I Q M A I R L Q A E G K T S L H K D L K Q K R R E Q R E Q R E
R R R A A K E B E L L R L Q Q L Q E E K E R K L Q E L L L Q E A Q R Q A E R L L Q E E H E R R R S
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L Q E A L Q L E V K A R R D E E S V R I A Q T R L L K E E E E K L K Q L M Q L K E E Q E R Y I E R A
Q Q E K E L L Q Q E M A Q Q S R S L Q Q A Q Q Q L E E V R Q N R Q R A D E D V E A A Q R K L R Q A S
T N V K H W N V Q M N R L M H P I E P G D E R P V T S S S F S G F Q P P L L A H R D S S L K R L T R
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Black = intracellular, Red = Transmembrane, Blue = Extracellular

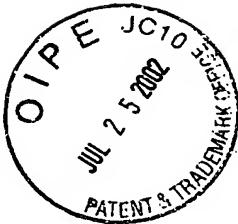
Ly1488Rp3-329A5Chr6 has 756 amino acids and 1 Transmembrane Domains
Transmembrane Domain 1: 199 - 220 Score: 1.3061



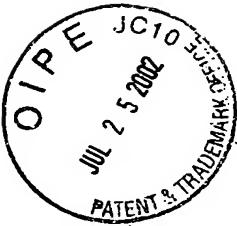
47/52

Ly1449 and Ly1480 matches Lung cancer associated
polynucleotide sequence SEQ ID 10,476

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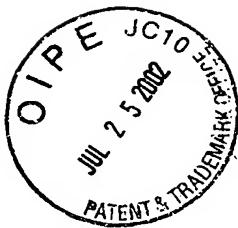


**Homo sapiens chromosome 17, clone RP11-956N15, complete sequence (bp1-10 000)
(SEQ ID NO: 10,474)**



49/52

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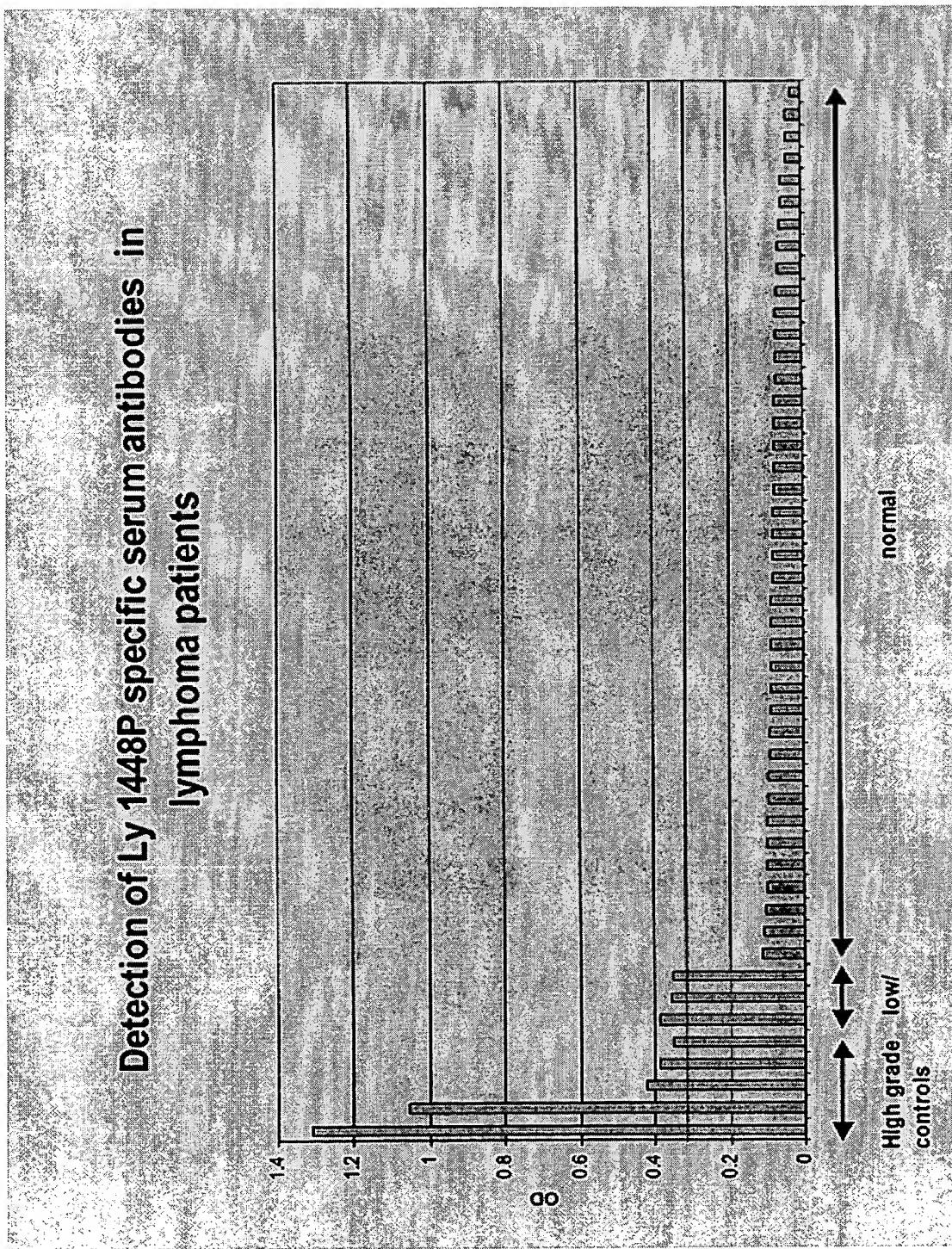
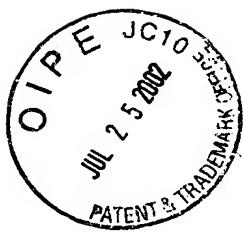
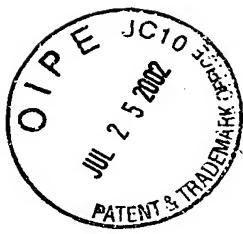


FIG. 31



Detection of TCL-1 specific serum antibodies in lymphoma patients

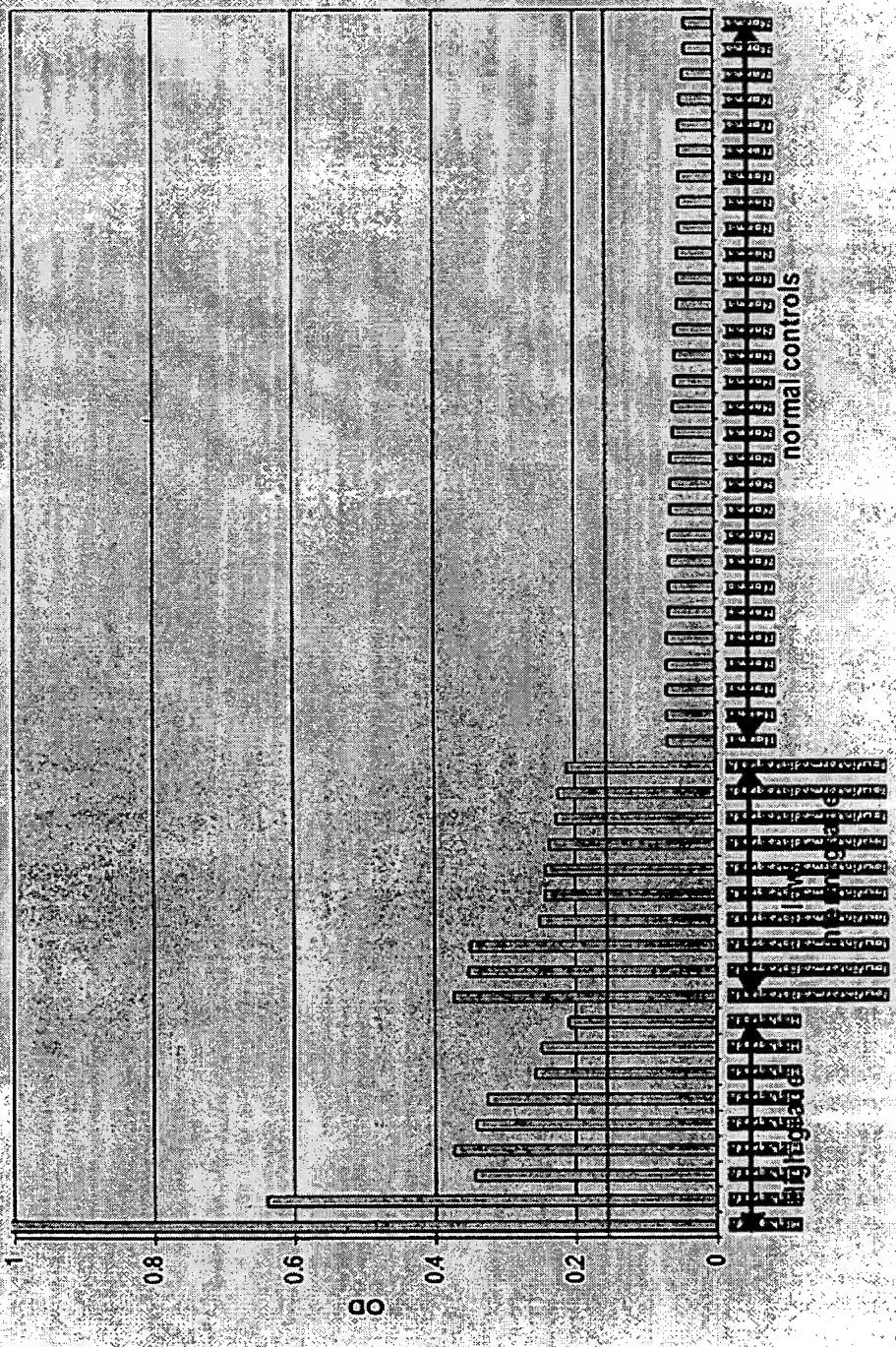
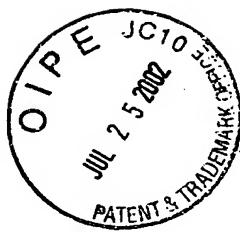


FIG. 32



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Detection of TCL-1 specific serum antibodies in lymphoma patients

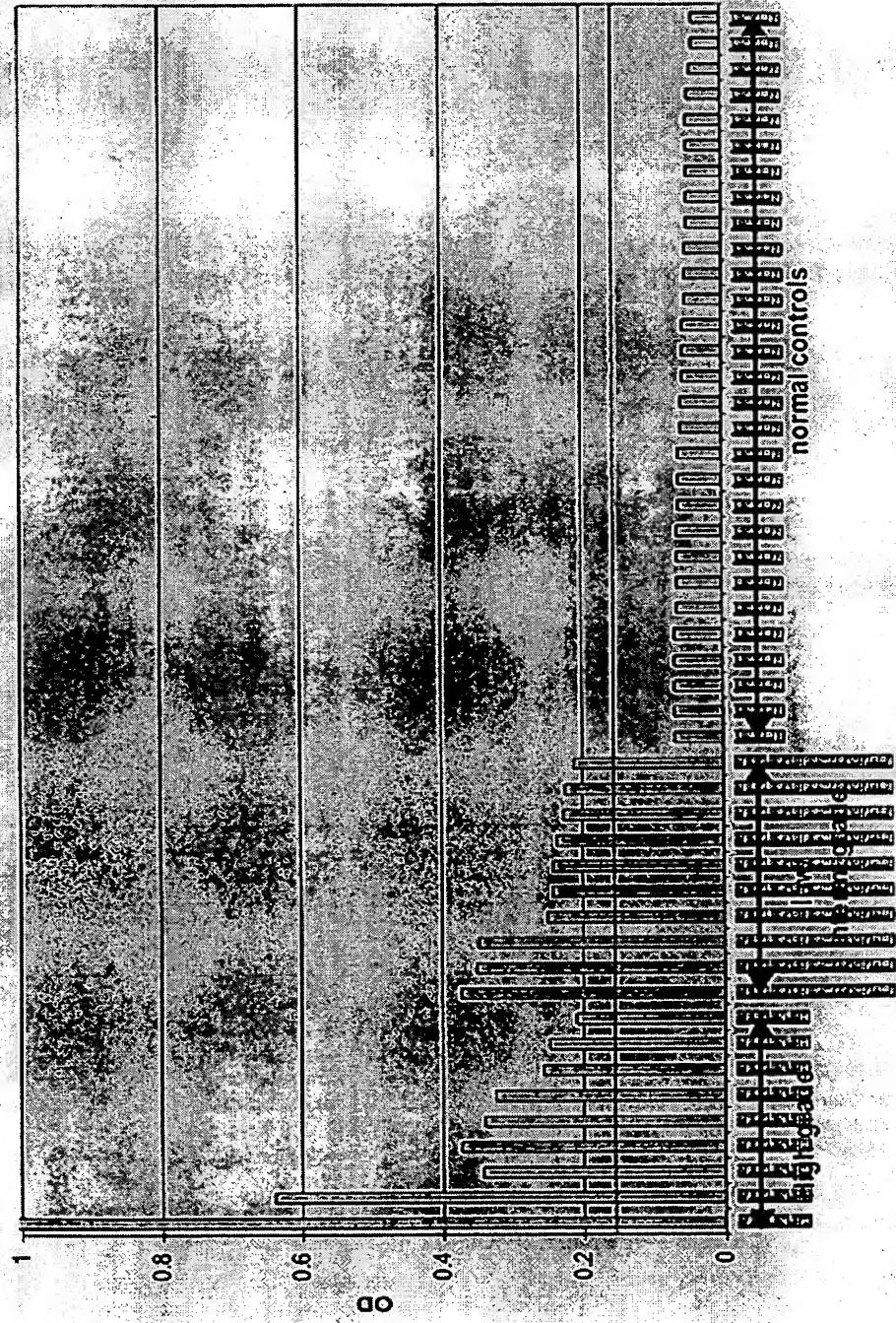


FIG. 32